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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:58:57 ; Search time 23 Seconds

(Without alignment)  
767.656 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EPHHHHTLSPSGPVTI.....HEALPGKTLKSLHYAAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents PA:\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989	53.3	426	1	US-08-336-583-2
2	989	53.3	426	5	PCT-US95-13795-2
3	972	52.4	431	4	US-09-479-614-14
4	972	52.4	496	4	US-09-479-614-2
5	972	52.4	496	4	US-09-479-614-29
6	673	36.3	561	3	US-09-192-545-2
7	579	31.2	113	2	US-08-232-539D-56
8	548.5	29.6	109	4	US-08-466-163B-1
9	548.5	29.6	109	4	US-09-802-096-1
10	538	29.0	106	2	US-08-232-539D-54
11	512	27.6	334	2	US-08-646-981-16
12	508	27.4	119	2	US-08-464-025A-1
13	501.5	27.0	331	2	US-08-646-981-17
14	492.5	26.5	450	2	US-08-788-800-12
15	492.5	26.5	469	2	US-07-934-373C-23
16	492.5	26.5	469	2	US-08-437-642B-23
17	492.5	26.5	469	4	US-08-146-206C-23
18	492.5	26.5	469	4	US-09-705-686-23
19	490.5	26.4	118	3	US-08-466-151-1
20	490	26.4	333	1	US-08-436-463-6
21	490	26.4	333	1	US-08-024-253-6
22	488	26.3	530	3	US-08-477-460B-4
23	488	26.3	530	3	US-08-379-516-4
24	488	26.3	530	3	US-09-329-916-4
25	488	26.3	530	3	US-08-485-372A-4
26	488	26.3	530	4	US-09-409-006A-4
27	488	26.3	530	4	US-08-484-681-4

28	488	26.3	530	5	PCT-US93-07422-4	Sequence 4, Appl
29	486.5	26.2	451	4	US-09-472-087-70	Sequence 70, Appl
30	486.5	26.2	463	4	US-09-472-087-1	Sequence 1, Appl
31	486.5	26.2	463	4	US-09-472-087-4	Sequence 4, Appl
32	486.5	26.2	463	4	US-09-472-087-63	Sequence 63, Appl
33	486.5	26.2	463	4	US-09-472-087-68	Sequence 68, Appl
34	486.5	26.2	464	4	US-09-472-087-2	Sequence 2, Appl
35	486.5	26.2	464	4	US-09-472-087-66	Sequence 66, Appl
36	480.5	25.9	463	4	US-09-472-087-64	Sequence 64, Appl
37	476.5	25.7	329	2	US-09-313-942-12	Sequence 12, Appl
38	476	25.6	337	4	US-08-761-272A-47	Sequence 47, Appl
39	476	25.6	443	5	PCT-US96-13152-4	Sequence 4, Appl
40	476	25.6	467	1	US-08-704-744-81	Sequence 81, Appl
41	476	25.6	467	3	US-08-523-894-8	Sequence 8, Appl
42	476	25.6	467	3	US-08-523-894-10	Sequence 10, Appl
43	476	25.6	467	3	US-08-523-894-12	Sequence 12, Appl
44	475.5	25.6	326	2	US-08-656-586-9	Sequence 9, Appl
45	468.5	25.2	552	5	PCT-US93-07832-23	Sequence 23, Appl

## ALIGNMENTS

```
RESULT 1
US-08-336-583-2
Sequence 2, Appl
Patent No. 5628415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: CHRISTINE E. CARY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2
Query Match 53.3%, Score 989, DB 1, Length 426;
Best Local Similarity 56.7%, Pred. No. 16-87;
Matches 185; Conservative 53; Mismatches 84; Indels 4; Gaps 3;
OY WTIPPTVTLFSSCGPBGDASTTOLCTVSGFSPAKVHWVWLVDSGAENLFPYTRP 77
DB 102 LNFIPPTVTLFSSCGPBGDASTTOLCTVSGFSPAKVHWVWLVDSGAENLFPYTRP 161
OY KRGQGTFLSGLSEVNTTQGMMSNTYTGCHVKNKSIIFEDSSKCAKADSNPRGVSAYLRP 137
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Db 162 TREGVNT-STHSELNITOGEMWSOKTYTCQVYOGFTKDEARKSESDEPRGVSTYLSPP 220  
Qy 138 SPFDLFIKRSPTITCLVVDLAPSKGTUWLTWSRASKGVNSTRKEEQRNGTLVSTL 197  
Db 221 SPDLVYHAKPKITCLVVDLATMEG-MNLTWRESKEPVPNGPLNKDHFNGITVSTL 279  
Qy 198 PVGTDMIGETGYOCVTHPHLPALMRSTYLPGRRLAPEVYMLPPSPETGTR--TV 255  
Db 280 PVNTDMIGETGYOCVTHPHLPKDIWRSIAAPGRAPDVYFLPPEEGOTKDRVTL 339  
Qy 256 TCLIRGEVPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDSPFLYSRLVYKSIWKN 315  
Db 340 TCLIQNFPPADISVQWLRNDSPIDQYTTTGPHKVSGRPAFLFSRLVSRVDMQKN 399  
Qy 316 LVTCRVVHEALPGSRITLKSILHYSAG 341  
Db 400 KFTCQVHHEALPGSRITLQKWSKTPG 425

## RESULT 2

PCT-US95-13795-2  
; Sequence 2, Application PC/TUS9513795  
; GENERAL INFORMATION:  
; APPLICANT: HOLLIS, GREGORY F.  
; APPLICANT: PATEL, MAYUR D.  
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHRISTINE E. CARTY  
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07065-0907  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13795  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARTY, CHRISTINE E.  
; REGISTRATION NUMBER: 36,099  
; REFERENCE/DOCKET NUMBER: 19211Y  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-6734  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-13795-2

Query Match 53.3%; Score 989; DB 5; Length 426;  
Best Local Similarity 56.7%; Pred. No. 1e-87;

Matches 185; Conservative 53; Mismatches 84; Indels 4; Gaps 3;

Qy 18 VTIIPTVTLFSSCCPRGDASTIQLCLVGFSPAKVHTWLVVDGQEAENLPYTRP 77  
Db 102 LNFIPPTVTLFSSCCNPVGDTHITITQLCLISGYPGMEVYTWLVGQKATNIPYTAG 161  
Qy 78 KREGGQFSLQSEVNITQGMSSNTYTCHVKNHSIFEDSRKCAQSNPGVSAVLSRP 137  
Db 162 TREGVNT-STHSELNITOGEMWSOKTYTCQVYOGFTKDEARKSESDEPRGVSTYLSPP 220  
Qy 138 SPFDLFIKRSPTITCLVVDLAPSKGTUWLTWSRASKGVNSTRKEEQRNGTLVSTL 197

Db 221 SPDLVYHAKPKITCLVVDLATMEG-MNLTWRESKEPVPNGPLNKDHFNGITVSTL 279  
Qy 198 PVGTDMIGETGYOCVTHPHLPALMRSTYLPGRRLAPEVYMLPPSPETGTR--TV 255  
Db 280 PVNTDMIGETGYOCVTHPHLPKDIWRSIAAPGRAPDVYFLPPEEGOTKDRVTL 339  
Qy 256 TCLIRGEVPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDSPFLYSRLVYKSIWKN 315  
Db 340 TCLIQNFPPADISVQWLRNDSPIDQYTTTGPHKVSGRPAFLFSRLVSRVDMQKN 399  
Qy 316 LVTCRVVHEALPGSRITLKSILHYSAG 341  
Db 400 KFTCQVHHEALPGSRITLQKWSKTPG 425

## RESULT 3

US-09-479-614-14  
; Sequence 14, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric  
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
; FILE REFERENCE: P-1047  
; CURRENT APPLICATION NUMBER: US/09/479,614  
; CURRENT FILING DATE: 2000-01-07  
; EARLIER APPLICATION NUMBER: 60/115,033  
; EARLIER FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-479-614-14

Query Match 52.4%; Score 972; DB 4; Length 431;  
Best Local Similarity 56.7%; Pred. No. 4.7e-86;

Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

Qy 18 VTIIPTVTLFSSCCPRGDASTIQLCLVGFSPAKVHTWLVVDGQEAENLPYTRP 77  
Db 107 LNFIPPTVTLFSSCCNPVGDTHITITQLCLISGYPGMEVYTWLVGQKATNIPYTAG 166  
Qy 78 KREGGQFSLQSEVNITQGMSSNTYTCHVKNHSIFEDSRKCAQSNPGVSAVLSRP 137  
Db 167 KREGVNT-STHSELNITOGEMWSOKTYTCQVYOGFTKDEARKSESDEPRGVSTYLSPP 225  
Qy 138 SPFDLFIKRSPTITCLVVDLAPSKGTUWLTWSRASKGVNSTRKEEQRNGTLVSTL 197  
Db 226 SPDLVYHAKPKITCLVVDLATMEG-MNLTWRESKEPVPNGPLNKDHFNGITVSTL 284  
Qy 198 PVGTDMIGETGYOCVTHPHLPALMRSTYLPGRRLAPEVYMLPPSPETGTR--TV 255  
Db 285 PVNTDMIGETGYOCVTHPHLPKDIWRSIAAPGRAPDVYFLPPEEGOTKDRVTL 344  
Qy 256 TCLIRGEVPSSEISVQWLFNNEEDHTGHTTTRPOKHGTDSPFLYSRLVYKSIWKN 315  
Db 345 TCLIQNFPPADISVQWLRNDSPIDQYTTTGPHKVSGRPAFLFSRLVSRVDMQKN 404  
Qy 316 LVTCRVVHEALPGSRITLKSILHYSAG 341  
Db 405 VFTCQVHHEALPGSRITLQKWSKTPG 425

## RESULT 4

US-09-479-614-2  
; Sequence 2, Application US/09479614  
; Patent No. 6573372  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine  
; APPLICANT: Weber, Eric

TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
 FILE REFERENCE: P-1047  
 CURRENT APPLICATION NUMBER: US/09/479,614  
 CURRENT FILING DATE: 2000-01-07  
 EARLIER APPLICATION NUMBER: 60/115,033  
 EARLIER FILING DATE: 1999-01-07  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 496  
 TYPE: PRT  
 ORGANISM: Felis catus  
 US-09-479-614-2

Query Match 52.4%; Score 972; DB 4; Length 496;  
 Best Local Similarity 56.7%; Pred. No. 5.8e-86;  
 Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

QY 18 VTIIPTVYKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVDOGAENLPYYTRP 77  
 DB 172 NMPIPTVYKLFHSSCNPLGDTSTIQLCLISGVYPGDMETWLVDOGAENLPYYTAPG 231  
 QY 78 KREGGQTFSLQSEVNTTQGMWSNTYTCVHKHNSIFEDSSRKCADNPRGVSAIYLRP 137  
 DB 232 KQEGKVT-STHSELNTQSEWVSQKTYTCQVYQGFTEEDARKCTESDPGVSTYLSPP 290  
 QY 138 SPFDLFIKSPITITCLVVDLAPSKGTVALTWASRASKPVNSTRKEKORNGTLVTSTL 197  
 DB 291 SPDLVYHKSFKITCLVVDLANTDGM1-LTWSRENGESVHPDPMVKKTQYNGITVTSTL 349  
 QY 198 PVGTRDMIGETVQCVTHPHLPRALMSTYTLPGKRLAPVYM-LPSPPE-ETGTTTIV 255  
 DB 350 PVDATDWEGEYQCKVTHPDLPKDIVRSIAAPGRPPRYVFLPPEGEKPKDKVTL 409  
 QY 256 TGLIRGFYSLSVQWLFNNBEDHTGHTTTRPOKHGTDSPSFLYSRMLVNSIWEKGN 315  
 DB 410 TGLIQNFPPDISVQWLFNDSFVTRTEQATWPHKATGSPAFVFSRLVEGRADWEQRD 469  
 QY 316 LVTGRVYHVALPGSRTLEKSLHYSAG 341  
 DB 470 VFTQVYHVALPGFRTLKKSVSKNPG 495

RESULT 5

US-09-479-614-29  
 Sequence 29, Application US/09479614  
 Patent No. 6573372  
 GENERAL INFORMATION:  
 APPLICANT: McCall, Catherine  
 APPLICANT: Weber, Eric  
 TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
 FILE REFERENCE: P-1047  
 CURRENT APPLICATION NUMBER: US/09/479,614  
 CURRENT FILING DATE: 2000-01-07  
 EARLIER APPLICATION NUMBER: 60/115,033  
 EARLIER FILING DATE: 1999-01-07  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 29  
 LENGTH: 496  
 TYPE: PRT  
 ORGANISM: Felis catus  
 US-09-479-614-29

Query Match 52.4%; Score 972; DB 4; Length 496;  
 Best Local Similarity 56.7%; Pred. No. 5.8e-86;  
 Matches 185; Conservative 52; Mismatches 85; Indels 4; Gaps 4;

QY 18 VTIIPTVYKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVDOGAENLPYYTRP 77  
 DB 172 NMPIPTVYKLFHSSCNPLGDTSTIQLCLISGVYPGDMETWLVDOGAENLPYYTAPG 231  
 QY 78 KREGGQTFSLQSEVNTTQGMWSNTYTCVHKHNSIFEDSSRKCADNPRGVSAIYLRP 137

DB 232 KQEGKVT-STHSELNTQSEWVSQKTYTCQVYQGFTEEDARKCTESDPGVSTYLSPP 290  
 QY 138 SPFDLFIKSPITITCLVVDLAPSKGTVALTWASRASKPVNSTRKEKORNGTLVTSTL 197  
 DB 291 SPDLVYHKSFKITCLVVDLANTDGM1-LTWSRENGESVHPDPMVKKTQYNGITVTSTL 349  
 QY 198 PVGTRDMIGETVQCVTHPHLPRALMSTYTLPGKRLAPVYM-LPSPPE-ETGTTTIV 255  
 DB 350 PVDATDWEGEYQCKVTHPDLPKDIVRSIAAPGRPPRYVFLPPEGEKPKDKVTL 409  
 QY 256 TGLIRGFYSLSVQWLFNNBEDHTGHTTTRPOKHGTDSPSFLYSRMLVNSIWEKGN 315  
 DB 410 TGLIQNFPPDISVQWLFNDSFVTRTEQATWPHKATGSPAFVFSRLVEGRADWEQRD 469  
 QY 316 LVTGRVYHVALPGSRTLEKSLHYSAG 341  
 DB 470 VFTQVYHVALPGFRTLKKSVSKNPG 495

RESULT 6

US-09-192-545-2  
 Sequence 2, Application US/09192545  
 Patent No. 6118044  
 GENERAL INFORMATION:  
 APPLICANT: Konekawa, Hajime  
 APPLICANT: Konekawa, Hiromichi  
 APPLICANT: Taya, Choji  
 APPLICANT: Matsuo, Kunie  
 TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use  
 FILE REFERENCE: 795P79570  
 CURRENT APPLICATION NUMBER: US/09/192,545  
 CURRENT FILING DATE: 1998-11-13  
 EARLIER APPLICATION NUMBER: JP HEI 9-313989  
 EARLIER FILING DATE: 1997-11-14  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 561  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: Description of Artificial Sequence: Designed heavy  
 US-09-192-545-2

Query Match 36.3%; Score 673; DB 3; Length 561;  
 Best Local Similarity 41.6%; Pred. No. 8.1e-57;  
 Matches 147; Conservative 53; Mismatches 133; Indels 20; Gaps 7;

QY 2 FHHHHHTLSLPESGVTIIPPTVYKLFHSSCDPRGDAHSTIQLCLVSGF 51  
 DB 211 FVCHVTHPSFESRTIIVRYT---HSLSPMSYSIHRCDPNA-FHSTIQLYCFYGH 265  
 QY 52 SPKAVHTWLVDOGAENLPYYTRPKRGGQTFSLQSEVNTTQGMWSNTYTCVHKH 111  
 DB 266 ILNDVSVSLMDRETDITLAQTVLKEE-GCLASTCKLNTTEQOMSESTFCRTVSO 324  
 QY 112 GELFEDSSRKCADNPRGVSAIYLRSPFDLFIKSPITITCLVVDLAPSKGTVALTWAS 171  
 DB 325 GVDYLAHTRKCPDHEKRAITLIPSPDLQNGAPFKTCLVLDSEK-VNNAVWNOE 383  
 QY 172 SGKPVNSTRKEKORNGTLVTSTLPVGTBDMIGETVQCVTHPHLPRALMSTYTL 231  
 DB 384 KKTYSVASQWYTKRHNNATITSITLIPVAKWIMIGYQCVVDRDPFKPIVRSIT-LP 442  
 QY 232 --GKLAPEVYMLPSPPEETGTRVYTCGLIRGFYSLSVQWLFNNBEDHTGHTTTRPQ 289  
 DB 443 QVQSASAEVYVFPPEESEDKRTITCLIQNFPPDISVQWLFNGKLISSQHSSTTLP 502  
 QY 290 KDHGTDSPSFLYSRMLVNSIWEKGNLVTGRVYHVALPGSRTLEKSLHYSAGN 342  
 DB 503 KNSGNSQGFIFSRLEVAKTWLTQKQFQVYHVALPKPRLEKTIISTISG 555

RESULT 7  
US-08-232-539D-56  
Sequence 56, Application US/08232539D  
Patent No. 5965709  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: IGE Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Syvoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9861  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 113 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-56  
Query Match 31.2%; Score 579; DB 2; Length 113;  
Best Local Similarity 98.2%; Pred. No. 1e-46;  
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CY 122 CADSNPRGVSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNSTR 181  
DB 1 CADSNPRGVSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNSTR 60  
CY 182 KEKORNGTLVTSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKLPg 232  
DB 61 KEKORNGTLVTSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKTSG 111  
RESULT 8  
US-08-466-163B-1  
Sequence 1, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P0718P2C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26

PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 1  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-466-163B-1  
Query Match 29.6%; Score 548.5; DB 4; Length 109;  
Best Local Similarity 97.2%; Pred. No. 8.9e-46;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
CY 124 DSNPRGVSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNSTRKE 183  
DB 1 DSNPRGVSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNSTRKE 60  
CY 184 EKORNGTLVTSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKLPg 232  
DB 61 EKORNGTLVTSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKTSG 108  
RESULT 9  
US-09-802-096-1  
Sequence 1, Application US/09802096  
Patent No. 6665939  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)  
FILE REFERENCE: P0718P2C3US  
CURRENT APPLICATION NUMBER: US/09/802,096  
FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: PCT/US92/06860  
PRIOR FILING DATE: 1992-08-14  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 1  
LENGTH: 109  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-802-096-1  
Query Match 29.6%; Score 548.5; DB 4; Length 109;  
Best Local Similarity 97.2%; Pred. No. 8.9e-46;  
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
CY 124 DSNPRGVSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNSTRKE 183  
DB 1 DSNPRGVSAVLSRSPFDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNSTRKE 60  
CY 184 EKORNGTLVTSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKLPg 232  
DB 61 EKORNGTLVTSTLPVGTDMIEGETYQCRVTHPHLPALMRSTTKTSG 108  
RESULT 10  
US-08-232-539D-54  
Sequence 54, Application US/08232539D  
Patent No. 5965709  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: IGE Antagonists

NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-232-539D-54

Query Match 29.0%; Score 538; DB 2; Length 106;  
Best Local Similarity 98.1%; Pred. No. 8.9e-45;  
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 129 GVSAYISRSPPDLFIRKSPITTCVVDLAPSKGTYNLTWSASGKPVNHSTRKEKOPN 188  
1 GVSAYISRSPPDLFIRKSPITTCVVDLAPSKGTYNLTWSASGKPVNHSTRKEKOPN 60

Qy 189 GILTVSTLPVGTBDWIEGEYQCRVTHPHLPALMRSTTKLPG 232  
61 GILTVSTLPVGTBDWIEGEYQCRVTHPHLPALMRSTTKISG 104

Db 129 GILTVSTLPVGTBDWIEGEYQCRVTHPHLPALMRSTTKLPG 232  
61 GILTVSTLPVGTBDWIEGEYQCRVTHPHLPALMRSTTKISG 104

RESULT 11  
US-08-646-981-16  
Sequence 16, Application US/08646981  
Patent No. 5852183  
GENERAL INFORMATION:  
APPLICANT: MAEDA, HIROAKI  
APPLICANT: EDA, YASUYUKI  
APPLICANT: KIMACHI, KAZUHIKO  
APPLICANT: ONO, YOICHI  
APPLICANT: TOKIYOSHI, SACHIO  
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE  
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE  
TITLE OF INVENTION: IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,981  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WEINER, MARC S  
REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 1488-106  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 334 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-646-981-16

Query Match 27.6%; Score 512; DB 2; Length 334;  
Best Local Similarity 35.9%; Pred. No. 1.7e-41;  
Matches 123; Conservative 60; Mismatches 122; Indels 38; Gaps 12;

Qy 23 PTVKLFHSQDPRGDHSTTQLCLVSGSEPAKYVHTW----LVDCQEAENLFPYTTTRK 78  
5 PVSFPLDPSG--STSGSTVALCLVSGYFPEPVVSMNSGSLTSG-----VHTFSPD 55

Qy 79 REGQTPSLQSEVNTIQGQMSNTYTCYKH-----NGSIFE--DSSRK 121  
56 LQSSGLYSLSNVTVPESRW--SSETPTONAHASTKTKVDKPKREKNGKVPFPDPCPC 114

Qy 122 CABSNGVSAVYSRSPFD-LFIRKSPITTCVVDLAPSKGTYNLTWSASGKPVNHG- 179  
115 PABMLGSPSVFTFPPEKDTLLIARTPEVTCVVDLGEDEPVCISWF-VGKQMQTAK 173

Qy 180 TRKEKORNGTLTVTSTLPVGTBDWIEGEYQCRVTHPHLPALMRSTTKLPKRLAPRY 239  
174 TQREBGFNTYVAVSLPIGHQDYLKQKQFTCKVNNKALPSIEITISKARQAHQPSV 233

Qy 240 YMLPSPER-TGTRVTVTCILIRGYPSEISVQMLFNNEEDHTGHTTTPQKDGTDPSE 298  
234 YVLPSPERE--SKNTVSLTCLIKDFFPPDIDVEQSGQEPESKRYTTPQDLE--DGSY 291

Qy 299 FLYSRMLVNSKIVKGNLTVCRVYHVALPGSRILESLHYSAG 341  
292 FLYSKLSYDKSRWQGDPTFCVAVHVALNHNHT-QKSLSHSPG 333

Db 299 FLYSRMLVNSKIVKGNLTVCRVYHVALPGSRILESLHYSAG 341  
292 FLYSKLSYDKSRWQGDPTFCVAVHVALNHNHT-QKSLSHSPG 333

RESULT 12  
US-08-464-025A-1  
Sequence 1, Application US/08464025A  
Patent No. 5994514  
GENERAL INFORMATION:  
APPLICANT: Jardieu et al.  
TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,025A  
FILING DATE: 05-Jun-1995  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Sueboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-464-025A-1

Query Match 27.4%; Score 508; DB 2; Length 119;  
Best Local Similarity 88.9%; Pred. No. 8.7e-42;  
Matches 104; Conservative 1; Mismatches 4; Indels 8; Gaps 4;

QY 124 DSNPRGVSAVLSRSPFDL-FIRKSPITICLVVDLAPSKGVNLTWSRAS--GKPVNHS 179  
DB 2 DSNPRGVSAVLSRSPFDLFIKSPITICLVVDLAPSKGVNLTWSRASXKGPVNH 61

QY 180 TREEKOR--NGLTVTSTLPVGRDMEGETYQCRVTHPHLPRAL-NRSTTKLPG 232  
DB 62 TREEKORXKXKSTLTVSTLPVGRDMEGETYQCRVTHPHLPRALXKRSITTKSG 118

RESULT 13  
US-08-646-981-17  
Sequence 17 Application US/08646981  
Patent No. 5852183  
GENERAL INFORMATION:  
APPLICANT: MAEDA, HIROAKI  
APPLICANT: EDA, YASUYUKI  
APPLICANT: KIMACHI, KAZUHIKO  
APPLICANT: ONO, YOICHI  
APPLICANT: TOKIYOSHI, SACHIO  
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE  
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE  
TITLE OF INVENTION: IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,981  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: WEINER, MARC S  
REGISTRATION NUMBER: 32,181  
REFERENCE/DOCKET NUMBER: 1488-106  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 331 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-646-981-17

Query Match 27.0%; Score 501.5; DB 2; Length 331;  
Best Local Similarity 36.3%; Pred. No. 1.7e-40;  
Matches 122; Conservative 62; Mismatches 125; Indels 27; Gaps 12;

QY 23 PTYKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVQGAENLPEYTTTPRKEG 82  
DB 5 PSYVPLAPSCG--STGSGTVTLACLIVSGYPEPVVSM-NSGSLTSGVHTFPVLKSSG- 60  
QY 83 QTFSLQSEVNILOQOMSSNTVTCVHKNS-----IFEDSSKRCADSN-----RG 129  
DB 61 -LVLSMTVTPSSR-LPSETICNVVHPATNTKVDKPGVPSKSTCKSLPCVPVSLGG 118  
QY 130 VSAYLSRSPFDL-FIRKSPITICLVVDLAPSKGVNLTWSRASGKPVNHS-TRKEKOR 187  
DB 119 PSYVFPPEPKDILIRITREVTQVLDLGRDEPEVQISWF-VDGKSVHTAKQPREQCF 177  
QY 188 NGULTVTSTLPVGRDMEGETYQCRVTHPHLPRALNRSTTKLPGKRLAPEVYMLPSPE 247  
DB 178 NSTYRVSVLPFIEHODWLTGKEFKCRVNHIGLPSPIERTISKRGQHQGVVLPSPSK 237  
QY 248 E--TGTTRVTVCLIRGYPSEISVQWLFNNEEDHTGHTTTPQKDHGTDPSFPLYSRL 305  
DB 238 ELSSDVTVTLCLIKOFFPEIDVEMQSNQPEPEKVTHTAQDDE--DGSYFLYSKLS 295  
QY 306 VNKSIWKEKMLVTCRVVHEALPESRTLEKSLHYSAG 341  
DB 296 VDKSRMEQDGFPCAVMEALQNHYT-DLSLHSPG 330

RESULT 14  
US-08-788-800-12  
Sequence 12 Application US/08788800  
Patent No. 5914112  
GENERAL INFORMATION:  
APPLICANT: Bednar, Martin M.  
APPLICANT: Thomas, G. Roger  
APPLICANT: Gross, Cordell E.  
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/788,800  
FILING DATE: 22-Jan-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0987r1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 450 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-788-800-12

Query Match 26.5%; Score 492.5; DB 2; Length 450;  
Best Local Similarity 36.5%; Pred. No. 2e-39;  
Matches 118; Conservative 57; Mismatches 119; Indels 29; Gaps 11;  
QY 35 RGDASHRTQLCLVSGSPAKVHTW---LVQGAENLPEYTTTPRKEGGQTFSLQSE 90

Db 140 RSTSESTALGCLVVDYFPEPVTVSMNGALTSG---VHTFPAVL-----QSSGLYSLSSV 192  
QY 91 VNITGQWMSNTYTCHVKG---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF 140  
Db 193 VVITSSNF-GTQYTCNVDHKPSNTKVDKTVRKCCEPCBPAPVAGPSVFLFPFKK 251  
QY 141 D-LFIRKSPITICLVVDLAPSKGTVNLWSPASGKPVNHSRKEKORNGTLTVSTLPV 199  
Db 252 DTLMISRTPEVTCVVDVSHEDPEVOFNWYVDGMEVHNAKTKPRBEQFNSTFRVSVLTV 311  
QY 200 GTRDWIEGTYOQRYTHPHLPALMRSTKLPGKRLAPEVYMLPPSPBE-TGTRTVCL 258  
Db 312 VHODWLNKGEYKCKVSNKGLPAPIEKTSKTKQPREPOVYTLPPSRBEKTKNOVSLTCL 371  
QY 259 IRGFYPSSEISVOMLNNEDHTGHHTTTPPOKHGTDPSPFLYSRMLVNSIWEKGNLTV 318  
Db 372 VKGFYPSDIAVWESNGOPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRMOQGNVFS 427  
QY 319 CRVHEALPGSRRTLEKSLHYSAG 341  
Db 428 CSVMHEALHNHT-OKSLSLSPG 449

## RESULT 15

US-07-934-373C-23  
; Sequence 23, Application US/07934373C  
; Patent No. 5821337  
; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Prestea  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 469 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-23

Query Match 26.5%; Score 492.5; DB 2; Length 469;  
Best Local Similarity 36.5%; Pred.No.2.2e-39;  
Matches 118; Conservative 57; Mismatches 119; Indels 29; Gaps 11;

QY 35 RGDASTITQLCLVSGSPAKVHTW---LVDOGAEANLEFYTTTPRKRGSGQTFSLQSE 90

Db 159 RSTSESTALGCLVVDYFPEPVTVSMNGALTSG---VHTFPAVL-----QSSGLYSLSSV 211  
QY 91 VNITGQWMSNTYTCHVKG---NGSIFEDSSRKCADSNP-----RGVSAYLSRPSPF 140  
Db 212 VVITSSNF-GTQYTCNVDHKPSNTKVDKTVRKCCEPCBPAPVAGPSVFLFPFKK 270  
QY 141 D-LFIRKSPITICLVVDLAPSKGTVNLWSPASGKPVNHSRKEKORNGTLTVSTLPV 199  
Db 271 DTLMISRTPEVTCVVDVSHEDPEVOFNWYVDGMEVHNAKTKPRBEQFNSTFRVSVLTV 330  
QY 200 GTRDWIEGTYOQRYTHPHLPALMRSTKLPGKRLAPEVYMLPPSPBE-TGTRTVCL 258  
Db 331 VHODWLNKGEYKCKVSNKGLPAPIEKTSKTKQPREPOVYTLPPSRBEKTKNOVSLTCL 390  
QY 259 IRGFYPSSEISVOMLNNEDHTGHHTTTPPOKHGTDPSPFLYSRMLVNSIWEKGNLTV 318  
Db 391 VKGFYPSDIAVWESNGOPEN--NYKTPPMLD--SDGSFFLYSKLTVDKSRMOQGNVFS 446  
QY 319 CRVHEALPGSRRTLEKSLHYSAG 341  
Db 447 CSVMHEALHNHT-OKSLSLSPG 468

Search completed: February 26, 2004, 12:04:43  
Job time : 25 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 11:59:57 : Search time 38 Seconds  
(without alignments)  
1900.379 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856  
Sequence: 1 EPHHHHTLSPESGPVTL.....HEALPGRTLEKSLHVSAGN 342

Scoring table: BLAST62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PT1_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PT05_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1856	100.0	342	9	US-09-401-636-8
2	1856	100.0	342	14	US-10-176-664-8
3	1644.5	88.6	341	9	US-09-401-636-11
4	1644.5	88.6	341	14	US-10-176-664-11
5	1587.5	85.5	341	9	US-09-401-636-3
6	1587.5	85.5	341	14	US-10-176-664-3
7	1587.5	85.5	345	9	US-09-401-636-10
8	1587.5	85.5	345	14	US-10-176-664-10
9	1568.5	84.5	341	9	US-09-401-636-9
10	1568.5	84.5	341	14	US-10-176-664-9
11	1553.5	83.7	341	9	US-09-401-636-4
12	1553.5	83.7	341	14	US-10-176-664-4
13	1528.5	82.4	341	9	US-09-401-636-6
14	1528.5	82.4	341	14	US-10-176-664-6
15	1523.5	82.1	446	14	US-10-214-524-32

Result No.	Score	Query Match %	Length	ID	Description
16	1519	81.8	342	9	US-09-401-636-5
17	1519	81.8	342	14	US-10-176-664-5
18	1285.5	69.3	427	14	US-10-214-524-36
19	1050.5	56.6	343	9	US-09-401-636-7
20	1050.5	56.6	343	14	US-10-176-664-7
21	1045.5	56.3	569	10	US-09-847-208-7
22	1044	56.2	577	14	US-10-214-524-29
23	1038.5	56.0	320	10	US-09-847-208-6
24	1038.5	56.0	323	9	US-09-949-375A-2
25	1038.5	56.0	323	9	US-09-949-375A-4
26	1038.5	56.0	323	9	US-09-949-375A-6
27	1038.5	56.0	331	9	US-09-401-636-1
28	1038.5	56.0	331	14	US-10-176-664-1
29	1038.5	56.0	331	14	US-10-207-655-329
30	1038.5	56.0	427	10	US-09-847-208-5
31	1038.5	56.0	428	9	US-09-916-230-1
32	1038.5	56.0	428	9	US-09-949-375A-1
33	1038.5	56.0	428	13	US-10-047-542-60
34	1038.5	56.0	574	13	US-10-047-542-45
35	1038.5	56.0	574	14	US-10-214-524-37
36	1038.5	56.0	574	14	US-10-050-962-176
37	1038.5	56.0	574	14	US-10-050-962-176
38	1038.5	56.0	592	14	US-10-207-655-334
39	1036.5	55.8	330	9	US-09-949-375A-10
40	1034.5	55.7	336	9	US-09-949-375A-8
41	1034.5	55.7	441	9	US-09-949-375A-7
42	1024.5	55.2	426	14	US-10-214-524-26
43	996.5	53.7	347	14	US-10-152-190-13
44	989	53.3	426	14	US-10-214-524-28
45	978	52.7	496	14	US-10-214-524-25

## ALIGNMENTS

```
RESULT 1
US-09-401-636-8
: Sequence 8, Application US/09401636
: Patent No. US20010038843A1
: GENERAL INFORMATION:
: APPLICANT: Hellman, Lars T.
: TITLE OF INVENTION: ENHANCED VACCINES
: FILE REFERENCE: 10923/006001
: CURRENT APPLICATION NUMBER: US/09/401,636
: PRIOR FILING DATE: 1999-09-22
: PRIOR APPLICATION NUMBER: US 60/106,652
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8
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Query Match 100.0% Score 1856; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-146;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPHHHHTLSPESGPVTLIPPTKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
Db 1 EPHHHHTLSPESGPVTLIPPTKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60
QY 61 LVDDGAEALFFYTRPRKRGQTSLQSEVNIITGOMSSNTTYCHYKXNGSIFEDSSR 120
Db 61 LVDDGAEALFFYTRPRKRGQTSLQSEVNIITGOMSSNTTYCHYKXNGSIFEDSSR 120
QY 121 KCADSNPRVSAVLSRPSFDFIRKSPITICLVVDLAPSKGTVALITWRASGKPVNST 180
Db 121 KCADSNPRVSAVLSRPSFDFIRKSPITICLVVDLAPSKGTVALITWRASGKPVNST 180
```



```

QY      181 RKEKQKNGTLVTSILPVGTRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
      181 RKEKQKNGTLVTSILPVGTRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
Db
QY      241 MLPSPPEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTRPKDGTDPSPFL 300
      241 MLPSPPEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTRPKDGTDPSPFL 300
Db
QY      301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
      301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
Db

```

```

RESULT 2
US-10-176-664-8
; Sequence 8, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-8

```

```

Query Match      100.0%; Score 1856; DB 14; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,4e-146;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EFHHHHHTLSLPESGPTTIIPTVYKLFHSSCDPRGDASTTQLCLVSGFSPAKVHYTW 60
      1 EFHHHHHTLSLPESGPTTIIPTVYKLFHSSCDPRGDASTTQLCLVSGFSPAKVHYTW 60
Db
QY      61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
      61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
Db
QY      121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLTWRSAGKPVNHST 180
      121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLTWRSAGKPVNHST 180
Db
QY      181 RKEKQKNGTLVTSILPVGTRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
      181 RKEKQKNGTLVTSILPVGTRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
Db
QY      241 MLPSPPEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTRPKDGTDPSPFL 300
      241 MLPSPPEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTRPKDGTDPSPFL 300
Db
QY      301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
      301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
Db

```

```

RESULT 3
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES

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; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

```

```

Query Match      88.6%; Score 1644.5; DB 9; Length 341;
Best Local Similarity 88.0%; Pred. No. 6.2e-129;
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

```

```

QY      1 EFHHHHHTLSLPESGPTTIIPTVYKLFHSSCDPRGDASTTQLCLVSGFSPAKVHYTW 60
      1 EFHHHHHTLSLPESGPTTIIPTVYKLFHSSCDPRGDASTTQLCLVSGFSPAKVHYTW 60
Db
QY      61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
      61 LVDCQEAENLFPYTRPKREGGQTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120
Db
QY      121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLTWRSAGKPVNHST 180
      121 KCADSNPRGVSAVLSRSPFDLFIKRSPTITCLVVDLADSKGTVNLTWRSAGKPVNHST 180
Db
QY      181 RKEKQKNGTLVTSILPVGTRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
      181 RKEKQKNGTLVTSILPVGTRDMIGETVQCRVTHPHLPALMRSTTLPGKRLAPEVY 240
Db
QY      241 MLPSPPEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTRPKDGTDPSPFL 300
      241 MLPSPPEETGTRTVCLIRGFYPSSEISVQWLFNNEEDHTGHTTTTRPKDGTDPSPFL 300
Db
QY      301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
      301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAGN 342
Db

```

```

RESULT 4
US-10-176-664-11
; Sequence 11, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

```

```

Query Match      88.6%; Score 1644.5; DB 14; Length 341;
Best Local Similarity 88.0%; Pred. No. 6.2e-129;
Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;
QY      1 EFHHHHHTLSLPESGPTTIIPTVYKLFHSSCDPRGDASTTQLCLVSGFSPAKVHYTW 60

```

```
Db 1 EPHHHHTLSPSSGPTTIPPTVKLFHSSCDPRGASHSTIQLCLVSGSPAKVHTW 60
Qy 61 LVDGQEAENLPPTTRPRREGGQTFSLQSEVNITQGMMSNTYTCVKNGSIFEDSSR 120
Db 61 LVDGQEAENLPPTTRPRREGGQTFSLQSEVNITQGMMSNTYTCVKNGSIFEDSSR 120
Qy 121 KCADSNPRGSAVYLSRPSFPLFIRKSPITTCVVDLAPSGKVTNLWMSASGKPVNHS 180
Db 121 KCSSDPRGVTSLSPSPDLVYHAKPKITCLVVDLAMEG-MULTWYKESKEPVNPG 179
Qy 181 RKEEKORNGTLVTSTLPVGRDMEIGETVQCRVTHPLPALMRSTTKLPGKRLAPEVY 240
Db 180 LNKDHFNGITTVSTLPVNTDMEIGETVQCRVTHPLPALMRSTTKLPGKRLAPEVY 239
Qy 241 MLPSPEETGTRVTCIRGFYSEISVQWLFNNEBDHGHHTTTRPOKHGTDPSFPL 300
Db 240 MLPSPEETGTRVTCIRGFYSEISVQWLFNNEBDHGHHTTTRPOKHGTDPSFPL 299
Qy 301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRILEKSLHYSAQN 342
Db 300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRILEKSLHYSAQN 341

RESULT 5
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match 85.5%; Score 1587.5; DB 9; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.5e-124;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

Qy 1 EPHHHHTLSPSSGPTTIPPTVKLFHSSCDPRGASHSTIQLCLVSGSPAKVHTW 60
Db 1 EPHHHHTLSPSSGPTTIPPTVKLFHSSCDPRGASHSTIQLCLVSGSPAKVHTW 60
Qy 61 LVDGQEAENLPPTTRPRREGGQTFSLQSEVNITQGMMSNTYTCVKNGSIFEDSSR 120
Db 61 LVDGQEAENLPPTTRPRREGGQTFSLQSEVNITQGMMSNTYTCVKNGSIFEDSSR 120
Qy 121 KCADSNPRGSAVYLSRPSFPLFIRKSPITTCVVDLAPSGKVTNLWMSASGKPVNHS 180
Db 121 KCSDTPRGISAVYLPPTODLFVKKVPITIGCLLVDA-SAEVNTWMSRESGQPVNPS 179
Qy 181 RKEEKORNGTLVTSTLPVGRDMEIGETVQCRVTHPLPALMRSTTKLPGKRLAPEVY 240
Db 180 LVVKEQVNGITVYSHLPVNTDMEIGETVQCRVTHPLPALMRSTTKLPGKRLAPEVY 239
Qy 241 MLPSPEETGTRVTCIRGFYSEISVQWLFNNEBDHGHHTTTRPOKHGTDPSFPL 300
Db 240 MLPSPEETGTRVTCIRGFYSEISVQWLFNNEBDHGHHTTTRPOKHGTDPSFPL 299
Qy 301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRILEKSLHYSAQN 342
Db 300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRILEKSLHYSAQN 341
```

```
RESULT 6
US-10-176-664-3
; Sequence 3, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-3

Query Match 85.5%; Score 1587.5; DB 14; Length 341;
Best Local Similarity 85.4%; Pred. No. 3.5e-124;
Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

Qy 1 EPHHHHTLSPSSGPTTIPPTVKLFHSSCDPRGASHSTIQLCLVSGSPAKVHTW 60
Db 1 EPHHHHTLSPSSGPTTIPPTVKLFHSSCDPRGASHSTIQLCLVSGSPAKVHTW 60
Qy 61 LVDGQEAENLPPTTRPRREGGQTFSLQSEVNITQGMMSNTYTCVKNGSIFEDSSR 120
Db 61 LVDGQEAENLPPTTRPRREGGQTFSLQSEVNITQGMMSNTYTCVKNGSIFEDSSR 120
Qy 121 KCADSNPRGSAVYLSRPSFPLFIRKSPITTCVVDLAPSGKVTNLWMSASGKPVNHS 180
Db 121 KCSDTPRGISAVYLPPTODLFVKKVPITIGCLLVDA-SAEVNTWMSRESGQPVNPS 179
Qy 181 RKEEKORNGTLVTSTLPVGRDMEIGETVQCRVTHPLPALMRSTTKLPGKRLAPEVY 240
Db 180 LVVKEQVNGITVYSHLPVNTDMEIGETVQCRVTHPLPALMRSTTKLPGKRLAPEVY 239
Qy 241 MLPSPEETGTRVTCIRGFYSEISVQWLFNNEBDHGHHTTTRPOKHGTDPSFPL 300
Db 240 MLPSPEETGTRVTCIRGFYSEISVQWLFNNEBDHGHHTTTRPOKHGTDPSFPL 299
Qy 301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRILEKSLHYSAQN 342
Db 300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRILEKSLHYSAQN 341

RESULT 7
US-09-401-636-10
; Sequence 10, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Artificial Sequence
```

FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-10

Query Match 85.5%; Score 1587.5; DB 9; Length 345;  
Best Local Similarity 84.7%; Pred. No. 3.5e-124;  
Matches 298; Conservative 14; Mismatches 23; Indels 17; Gaps 4;

QY 1 EFNHHHHTLSLPSGPGVTIIPPTVGLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60  
DB 1 EFNHHHHTLSLPSGPGVTIIPPTVGLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60  
QY 61 LVDGQAEMLFPYTPTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120  
DB 61 LVDGQAEMLFPYTPTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120  
QY 121 KC-ADSNPRGVSAVLSRPSPELFIKSPITICLVADLPSKGTVNLTSRAS----- 172  
DB 121 KCTAEBEPGVSAVLSRPSPELFIKSPITICLVADLPSKGTVNLTSRAS----- 172  
QY 173 --GKPVNSTRKEKQKNGTLVTSTLPGTRDMEGETYQCRVTHPHLPALMRSTTKL 230  
DB 180 PRGPV-----IKPQNGTFSATSTLPVNSDMIEGETYCNVTHPDLPKILRSISKL 233  
QY 231 PGKRLAPEVYMLPPSPEETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 290  
DB 234 PGKRLAPEVYMLPPSPEETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 293  
QY 291 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342  
DB 294 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 345

RESULT 8  
US-10-176-664-10  
Sequence 10, Application US/10176664  
Publication No. US20030031663A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/10/176,664  
CURRENT FILING DATE: 2002-06-19  
PRIOR APPLICATION NUMBER: US/09/401,636  
PRIOR FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 345  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-10-176-664-10

Query Match 85.5%; Score 1587.5; DB 14; Length 345;  
Best Local Similarity 84.7%; Pred. No. 3.5e-124;  
Matches 298; Conservative 14; Mismatches 23; Indels 17; Gaps 4;

QY 1 EFNHHHHTLSLPSGPGVTIIPPTVGLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60  
DB 1 EFNHHHHTLSLPSGPGVTIIPPTVGLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60  
QY 61 LVDGQAEMLFPYTPTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120  
DB 61 LVDGQAEMLFPYTPTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120  
QY 121 KC-ADSNPRGVSAVLSRPSPELFIKSPITICLVADLPSKGTVNLTSRAS----- 172  
DB 121 KCTAEBEPGVSAVLSRPSPELFIKSPITICLVADLPSKGTVNLTSRAS----- 179

QY 173 --GKPVNSTRKEKQKNGTLVTSTLPGTRDMEGETYQCRVTHPHLPALMRSTTKL 230  
DB 180 PRGPV-----IKPQNGTFSATSTLPVNSDMIEGETYCNVTHPDLPKILRSISKL 233  
QY 231 PGKRLAPEVYMLPPSPEETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 290  
DB 234 PGKRLAPEVYMLPPSPEETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOK 293  
QY 291 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342  
DB 294 DHGTDSPFLYSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 345

RESULT 9  
US-09-401-636-9  
Sequence 9, Application US/09401636  
Patent No. US20010038643A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/09/401,636  
CURRENT FILING DATE: 1999-09-22  
PRIOR APPLICATION NUMBER: US 60/106,652  
PRIOR FILING DATE: 1998-11-02  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 341  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated proteins  
US-09-401-636-9

Query Match 84.5%; Score 1568.5; DB 9; Length 341;  
Best Local Similarity 83.3%; Pred. No. 1.3e-122;  
Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 EFNHHHHTLSLPSGPGVTIIPPTVGLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60  
DB 1 EFNHHHHTLSLPSGPGVTIIPPTVGLFHSSCDPRDASTIQLCLVSGSPAKVHTW 60  
QY 61 LVDGQAEMLFPYTPTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120  
DB 61 LVDGQAEMLFPYTPTRPKRGQGFSLQSEVNITQGMMSNTYTCHVGNISIFEDSSR 120  
QY 121 KCADSNPRGVSAVLSRPSPELFIKSPITICLVADLPSKGTVNLTSRASGKPVNHT 180  
DB 121 RCDSDERGVITLIPSPPLDLYENGTGPKLTVADL--SEENITVWVERKKSIGSAS 179  
QY 181 RKEKQKNGTLVTSTLPGTRDMEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVY 240  
DB 180 QRETKHNAATSTISLIPVDAKMIEGEGQCKVDHPHPKPIVRSITLPGKRLAPEVY 239  
QY 241 MLPPSPEETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOKHGTDSPFL 300  
DB 240 MLPPSPEETGTRTVCLIRGFPSISVQWLFNNEEDHTGHTTTRPOKHGTDSPFL 299  
QY 301 YSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 342  
DB 300 YSRMLVNSKIWEKGNLVTCRVVHEALPGSRITLKSLSHYSAGN 341

RESULT 10  
US-10-176-664-9  
Sequence 9, Application US/10176664  
Publication No. US20030031663A1  
GENERAL INFORMATION:  
APPLICANT: Hellman, Lars T.  
TITLE OF INVENTION: ENHANCED VACCINES  
FILE REFERENCE: 10223/006001  
CURRENT APPLICATION NUMBER: US/10/176,664

CURRENT FILING DATE: 2002-06-19  
 PRIOR APPLICATION NUMBER: US/09/401,636  
 PRIOR FILING DATE: 1999-09-22  
 PRIOR APPLICATION NUMBER: US 60/106,652  
 PRIOR FILING DATE: 1998-11-02  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 9  
 LENGTH: 341  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetically generated proteins  
 US-10-176-664-9

Query Match 84.5%; Score 1568.5; DB 14; Length 341;  
 Best Local Similarity 83.3%; Pred. No. 1,3e-122;  
 Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 QY 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITGGWMSNTYTCVKNKNSIFEDSSR 120  
 DB 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITGGWMSNTYTCVKNKNSIFEDSSR 120  
 QY 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSKGTNVLWRSRAGKPVNHS 180  
 DB 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSKGTNVLWRSRAGKPVNHS 180  
 QY 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVTVWRKKSIGSAS 179  
 DB 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVTVWRKKSIGSAS 179  
 QY 181 RKEEKORNGTLVTSTLPVGRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240  
 DB 181 RKEEKORNGTLVTSTLPVGRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240  
 QY 180 ORSTKHNAVTSTISILPVDAKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239  
 DB 180 ORSTKHNAVTSTISILPVDAKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239  
 QY 241 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 300  
 DB 241 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 300  
 QY 240 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 299  
 DB 240 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 299  
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 QY 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341  
 DB 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

## RESULT 11

US-09-401-636-4  
 Sequence 4, Application US/09401636  
 Patent No. US2001003843A1  
 GENERAL INFORMATION:  
 APPLICANT: Hellman, Lars T.  
 TITLE OF INVENTION: ENHANCED VACCINES  
 FILE REFERENCE: 10223/006001  
 CURRENT APPLICATION NUMBER: US/09/401,636  
 CURRENT FILING DATE: 1999-09-22  
 PRIOR APPLICATION NUMBER: US 60/106,652  
 PRIOR FILING DATE: 1998-11-02  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 4  
 LENGTH: 341  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetically generated proteins  
 US-09-401-636-4

Query Match 83.7%; Score 1553.5; DB 9; Length 341;  
 Best Local Similarity 82.7%; Pred. No. 2.4e-121;  
 Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60

QY 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITGGWMSNTYTCVKNKNSIFEDSSR 120  
 DB 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITGGWMSNTYTCVKNKNSIFEDSSR 120  
 QY 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSKGTNVLWRSRAGKPVNHS 180  
 DB 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSKGTNVLWRSRAGKPVNHS 180  
 QY 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVTVWRKKSIGSAS 179  
 DB 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVTVWRKKSIGSAS 179  
 QY 181 RKEEKORNGTLVTSTLPVGRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240  
 DB 181 RKEEKORNGTLVTSTLPVGRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240  
 QY 180 ORSTKHNAVTSTISILPVDAKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239  
 DB 180 ORSTKHNAVTSTISILPVDAKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239  
 QY 241 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 300  
 DB 241 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 300  
 QY 240 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 299  
 DB 240 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 299  
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 QY 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341  
 DB 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

## RESULT 12

US-10-176-664-4  
 Sequence 4, Application US/10176664  
 Publication No. US20030031663A1  
 GENERAL INFORMATION:  
 APPLICANT: Hellman, Lars T.  
 TITLE OF INVENTION: ENHANCED VACCINES  
 FILE REFERENCE: 10223/006001  
 CURRENT APPLICATION NUMBER: US/10/176,664  
 CURRENT FILING DATE: 2002-06-19  
 PRIOR APPLICATION NUMBER: US/09/401,636  
 PRIOR FILING DATE: 1999-09-22  
 PRIOR APPLICATION NUMBER: US 60/106,652  
 PRIOR FILING DATE: 1998-11-02  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 4  
 LENGTH: 341  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Synthetically generated proteins  
 US-10-176-664-4

Query Match 83.7%; Score 1553.5; DB 14; Length 341;  
 Best Local Similarity 82.7%; Pred. No. 2.4e-121;  
 Matches 283; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

QY 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 DB 1 EFHHHHHTLSLPESGPTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 QY 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITGGWMSNTYTCVKNKNSIFEDSSR 120  
 DB 61 LVDGGAENLFPYTRPRKGGQTSLOSEVNITGGWMSNTYTCVKNKNSIFEDSSR 120  
 QY 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSKGTNVLWRSRAGKPVNHS 180  
 DB 121 KCADSNPRGSAVLSRSPFDLFIKSPITICLVLDAPSKGTNVLWRSRAGKPVNHS 180  
 QY 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVTVWRKKSIGSAS 179  
 DB 121 RCDSDPRGVITVTLIPSPDLVYENGTPKLCVLDL-ESEENITVTVWRKKSIGSAS 179  
 QY 181 RKEEKORNGTLVTSTLPVGRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240  
 DB 181 RKEEKORNGTLVTSTLPVGRDWEGETYQCRVTHPHLPALMRSTTKLPKRLAPEVY 240  
 QY 180 ORSTKHNAVTSTISILPVDAKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239  
 DB 180 ORSTKHNAVTSTISILPVDAKWIIEGEGYQCRVDHPHPKPIVASITKLPKRLAPEVY 239  
 QY 241 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 300  
 DB 241 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 300  
 QY 240 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 299  
 DB 240 MLPSPPEETGTRVTCILRGFYPSIEISVQWLFNNEEDHTGHTTTPQKHGTDPSFPL 299  
 QY 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 QY 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341  
 DB 300 YSRMLVNKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 13  
US-09-401-636-6

Sequence 6, Application US/09401636  
Patent No. US20010038843A1

GENERAL INFORMATION:

APPLICANT: Heliman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/09/401,636

CURRENT FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 341

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Synthetically generated proteins

US-09-401-636-6

Query Match 82.4%; Score 1528.5; DB 9; Length 341;  
Best Local Similarity 83.0%; Pred. No. 2,9e-119;  
Matches 284; Conservative 14; Mismatches 43; Indels 1; Gaps 1;

```

QY 1 EHHHHHHHTLSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHYTM 60
DB 1 EHHHHHHHTLSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHYTM 60
QY 61 LVDCGAEMLFPPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDCGAEMLFPPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFIKSPFTITCLVVDLAPSKGTNLTWSRASGKPVNHS 180
DB 121 KCADSNPRGSAVLSRSPFDLFIKSPFTITCLVVDLAPSKGTNLTWSRASGKPVNHS 180
QY 121 RCPDHEPRGVIITLIPSPDLVYONGAPKLTCLVVDLSEK-NVNTWNOEKKTSVNASQ 179
DB 121 RCPDHEPRGVIITLIPSPDLVYONGAPKLTCLVVDLSEK-NVNTWNOEKKTSVNASQ 179
QY 181 RKEBKORNGTLVTSITLIPVAKDMIGYQICVDHPDPKPIVRSITLPGKRLAPEVY 240
DB 181 RKEBKORNGTLVTSITLIPVAKDMIGYQICVDHPDPKPIVRSITLPGKRLAPEVY 240
QY 241 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 300
DB 241 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 300
QY 240 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 299
DB 240 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 299
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342

```

RESULT 14

US-10-176-664-6

Sequence 6, Application US/10176664

Publication No. US20030031663A1

GENERAL INFORMATION:

APPLICANT: Heliman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/10/176,664

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 341

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Synthetically generated proteins

US-10-176-664-6

Query Match 82.4%; Score 1528.5; DB 14; Length 341;

Best Local Similarity 83.0%; Pred. No. 2,9e-119;

Matches 284; Conservative 14; Mismatches 43; Indels 1; Gaps 1;

```

QY 1 EHHHHHHHTLSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHYTM 60
DB 1 EHHHHHHHTLSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHYTM 60
QY 61 LVDCGAEMLFPPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVKNKNGSIFEDSSR 120
DB 61 LVDCGAEMLFPPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVKNKNGSIFEDSSR 120
QY 121 KCADSNPRGSAVLSRSPFDLFIKSPFTITCLVVDLAPSKGTNLTWSRASGKPVNHS 180
DB 121 KCADSNPRGSAVLSRSPFDLFIKSPFTITCLVVDLAPSKGTNLTWSRASGKPVNHS 180
QY 121 RCPDHEPRGVIITLIPSPDLVYONGAPKLTCLVVDLSEK-NVNTWNOEKKTSVNASQ 179
DB 121 RCPDHEPRGVIITLIPSPDLVYONGAPKLTCLVVDLSEK-NVNTWNOEKKTSVNASQ 179
QY 181 RKEBKORNGTLVTSITLIPVAKDMIGYQICVDHPDPKPIVRSITLPGKRLAPEVY 240
DB 181 RKEBKORNGTLVTSITLIPVAKDMIGYQICVDHPDPKPIVRSITLPGKRLAPEVY 240
QY 241 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 300
DB 241 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 300
QY 240 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 299
DB 240 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 299
QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342
DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRITLSEKSLHYAGN 342

```

RESULT 15

US-10-214-524-32

Sequence 32, Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:

APPLICANT: Chen, Swey-Shen Alex

APPLICANT: Yang, Yong-Min

APPLICANT: Barankiewicz, Theresa J.

APPLICANT: Chen, Zhong

TITLE OF INVENTION: IMMUNOLOGICAL VACCINES AND METHODS OF USE THEREOF

FILE REFERENCE: IGE-00101.P.1.1

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08

PRIOR APPLICATION NUMBER: 60/312,120

PRIOR FILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patent version 3.1

SEQ ID NO 32

LENGTH: 446

TYPE: PRT

ORGANISM: Opossum (Monodelphis domestica)

US-10-214-524-32

Query Match 82.1%; Score 1523.5; DB 14; Length 446;  
Best Local Similarity 84.7%; Pred. No. 1.1e-118;

Matches 283; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

```

QY 9 TSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHYTM 68
DB 114 TSLPESGPTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHYTM 68
QY 69 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 128
DB 174 MLPSPETGTRTTCVCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFPL 128
QY 129 GVSAYLSRSPFDLFIKSPFTITCLVVDLAPSKGTNLTWSRASGKPVNHSSTRKEKOR 188
DB 234 GVSAYLSRSPFDLFIKSPFTITCLVVDLAPSKGTNLTWSRASGKPVNHSSTRKEKOR 188
QY 189 GITLVTSITLIPVAKDMIGYQICVDHPDPKPIVRSITLPGKRLAPEVY 248
DB 189 GITLVTSITLIPVAKDMIGYQICVDHPDPKPIVRSITLPGKRLAPEVY 248

```

Db	293	GFFTVTSHPVNTDWMIEGDITTCRLSPDMVPLIRITISKAPGRLAPEVYMLPSPPEE	352
Qy	249	TGTRTVTCLIRGFPSPSISVOMLPNNEDHTGHTTTRPOKDGTDPSPFLYSRMLVNK	308
Db	353	TGTRTVTCLIRGFPSPSISVOMLPNNEDHTGHTTTRPOKDGTDPSPFLYSRMLVNK	412
Qy	309	SIMEKGNLVTCEVVEALPGSRTLEKSLHYSAGN	342
Db	413	SIMEKGNLVTCEVVEALPGSRTLEKSLHYSAGN	446

Search completed: February 26, 2004, 12:05:55  
 Job time : 39 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2004, 11:42:41 ; Search time 59 seconds  
(without alignments)  
1637.818 Million cell updates/sec

Title: US-09-401-636-8  
Perfect score: 1856  
Sequence: 1 EFHHHHHTLSPESGPVTI.....HEALPGSRLEKSLHYSGN 342

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_28Jan04:\*

- 1: geneSeq19808:\*
- 2: geneSeq19908:\*
- 3: geneSeq20008:\*
- 4: geneSeq20018:\*
- 5: geneSeq20028:\*
- 6: geneSeq20038:\*
- 7: geneSeq20038:\*
- 8: geneSeq20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1856	100.0	342 3 AAB06205	AAB06205 Immunogen
2	1644.5	88.6	341 3 AAB06208	AAB06208 Immunogen
3	1587.5	85.5	345 3 AAB06207	AAB06207 Immunogen
4	1584.5	85.4	341 3 AAB03644	AAB03644 Opossum I
5	1568.5	84.5	341 3 AAB06206	AAB06206 Opossum I
6	1523.5	82.1	446 6 ABP96587	ABP96587 Opossum I
7	1392.5	75.0	341 3 AAB06202	AAB06202 Immunogen
8	1375	74.1	342 3 AAB06201	AAB06201 Immunogen
9	1285.5	69.3	427 6 ABP96591	ABP96591 Brushtail
10	1045.5	56.3	569 6 ABP96584	ABP96584 Duckbill
11	1044	56.2	577 6 AAB03667	AAB03667 Human IGE
12	1038.5	56.0	320 6 AAB03667	AAB03667 Human IGE
13	1038.5	56.0	323 5 AAB080286	AAB080286 Human IGE
14	1038.5	56.0	323 5 AAB080285	AAB080285 Human IGE
15	1038.5	56.0	323 5 AAB080284	AAB080284 Human IGE
16	1038.5	56.0	324 2 AAB83559	AAB83559 FC(eps)110
17	1038.5	56.0	325 2 AAR75225	AAR75225 Human IGE
18	1038.5	56.0	325 2 AAR77241	AAR77241 Human IGE
19	1038.5	56.0	331 7 AAB03642	AAB03642 Human IGE
20	1038.5	56.0	331 7 AAD25768	AAD25768 Binding d
21	1038.5	56.0	367 1 AAB80291	AAB80291 Interleuk
22	1038.5	56.0	427 6 AAB019666	AAB019666 Human IGE
23	1038.5	56.0	428 5 AAB47863	AAB47863 Human IGE
24	1038.5	56.0	428 5 AAB080283	AAB080283 Human IGE
25	1038.5	56.0	428 5 AAM50940	AAM50940 Human IGE

26	1038.5	56.0	428 6 AAE35113	AAE35113 Human Imm
27	1038.5	56.0	428 7 AAD48440	AAD48440 Human Pro
28	1038.5	56.0	574 5 ABG94250	ABG94250 Human IGE
29	1038.5	56.0	574 5 ABG80562	ABG80562 Human IGE
30	1038.5	56.0	574 6 ABP96592	ABP96592 Human IGE
31	1038.5	56.0	592 7 AAD25773	AAD25773 Binding d
32	1036.5	55.8	330 5 AAB080289	AAB080289 Human IGE
33	1035.5	55.8	325 3 AAY79994	AAY79994 Human Imm
34	1034.5	55.7	431 5 AAB080287	AAB080287 Human IGE
35	1034.5	55.7	441 5 AAB080287	AAB080287 Human IGE
36	1030.5	55.5	493 1 AAP40065	AAP40065 Sequence
37	1024.5	55.2	426 6 ABP96581	ABP96581 Chimpanze
38	1019.5	54.9	315 2 AAB85582	AAB85582 CH2 to CH
39	1019.5	54.9	325 2 AAB83582	AAB83582 CH2 to CH
40	1010.5	54.4	425 6 AAE35114	AAE35114 Human Imm
41	1002.5	54.0	428 2 AAR42950	AAR42950 Human IGE
42	996.5	53.7	347 6 ABG74784	ABG74784 Human IGE
43	992.5	53.5	343 3 AAB06204	AAB06204 Dog IGE h
44	989	53.3	426 6 ABP96583	ABP96583 Dog IGE h
45	978	52.7	496 6 ABP96580	ABP96580 Cat IGE h

## ALIGNMENTS

RESULT 1  
AAB06205  
ID AAB06205 standard; protein; 342 AA.

AC AAB06205;  
XX

XX 12-SEP-2003 (revised)  
DT 22-NOV-2000 (first entry)  
XX

DE Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.  
XX

KW Human; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;  
KW atchma; eczema; immunogenic peptide.  
XX

OS Didelphis virginiana.  
OS Homo sapiens.  
OS Chimeric.  
XX

PN WO200025722-A2.  
XX

PD 11-MAY-2000.  
XX

PP 21-OCT-1999; 99WO-SE001896.  
XX

PR 02-NOV-1998; 98US-0106652P.  
PR 22-SEP-1999; 99US-00401636.  
XX

PA (RESI-) RESISTENTIA PHARM AB.  
XX

PI Helman LT;  
XX

DR WPI; 2000-365342/31.  
XX

PT Immunogenic polypeptides useful for preventing the harmful effects of  
PT immunoglobulin E in mammals.  
XX

PS Disclosure; Fig 2; 50pp; English.  
XX

XX The present sequence is an immunogenic peptide consisting of the heavy  
chain constant regions 2 and 4 of the opossum IGE and the heavy chain  
constant region 3 from the human. It was shown to cause a stronger  
polyclonal anti-self IGE response than peptides consisting of the same  
regions from one mammal. Immunogenic peptides, particularly those  
consisting of different heavy chain constant regions, can be used for  
vaccination in humans, against bacterial and viral infections and  
allergies, such as asthma, fur, pollen and food allergies and eczema.  
(Updated on 12-SEP-2003 to standardise OS field)  
XX

SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1856; DB 3; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-146;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPHHHHHHTLSLPSGSPVTTIIPPTVCLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 DB 1 EPHHHHHHTLSLPSGSPVTTIIPPTVCLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 QY 61 LVGGOAEHLNLFPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120  
 DB 61 LVGGOAEHLNLFPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAVLSRSPFDLFIKSPITTCIVDLAPSKGTNLTMSRASKPVNHST 180  
 DB 121 KCADSNPRGVSAVLSRSPFDLFIKSPITTCIVDLAPSKGTNLTMSRASKPVNHST 180  
 QY 181 RKEKQRNGTLVTSTLPVGTDRWINGETVYQCRVTHPHLPALMSTTKLPKRLAPEVY 240  
 DB 181 RKEKQRNGTLVTSTLPVGTDRWINGETVYQCRVTHPHLPALMSTTKLPKRLAPEVY 240  
 QY 241 MLPSPSEETGTRTVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKDHGTDPSFPL 300  
 DB 241 MLPSPSEETGTRTVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKDHGTDPSFPL 300  
 QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342

RESULT 2  
 AAB06208  
 ID AAB06208 standard; protein; 341 AA.  
 AC AAB06208;  
 DT 12-SEP-2003 (revised)  
 DT 22-NOV-2000 (first entry)  
 XX  
 DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.  
 XX  
 KM Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
 KM asthma; eczema; immunogenic peptide.  
 XX  
 OS Didelphis virginiana.  
 OS Canis sp.  
 OS Chimeric.  
 OS  
 XX WO200025722-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 21-OCT-1999; 99WO-SR001896.  
 XX  
 PR 02-NOV-1998; 98US-0106552P.  
 PR 22-SEP-1999; 99US-00401636.  
 XX  
 PA (RESI-) RESISTENTIA PHARM AB.  
 XX  
 PI Hellman LT;  
 XX  
 DR WPI; 2000-365342/31.  
 XX  
 PT Immunogenic polypeptides useful for preventing the harmful effects of  
 XX immunoglobulin E in mammals.  
 XX  
 PS Disclosure; Fig 2; 5opp; English.  
 XX  
 CC The present sequence is an immunogenic peptide consisting of the heavy  
 CC chain constant regions 2 and 4 of the opossum Igs and the heavy chain  
 CC constant region 3 from the dog. It was shown to cause a stronger  
 CC polyclonal anti-self IGF response than peptides consisting of the same

CC regions from one mammal. Immunogenic peptides, particularly those  
 CC consisting of different heavy chain constant regions, can be used for  
 CC vaccination in humans, against bacterial and viral infections and  
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.  
 CC (Updated on 12-SEP-2003 to standardise OS field)  
 CC  
 XX  
 SQ Sequence 341 AA;  
 Query Match 88.6%; Score 1644.5; DB 3; Length 341;  
 Best Local Similarity 88.0%; Pred. No. 1.6e-128;  
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EPHHHHHHTLSLPSGSPVTTIIPPTVCLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 DB 1 EPHHHHHHTLSLPSGSPVTTIIPPTVCLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTW 60  
 QY 61 LVGGOAEHLNLFPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120  
 DB 61 LVGGOAEHLNLFPTTPKREGGOTFSLQSEVNITQGMSSNTYTCVHNGSIFEDSSR 120  
 QY 121 KCADSNPRGVSAVLSRSPFDLFIKSPITTCIVDLAPSKGTNLTMSRASKPVNHST 180  
 DB 121 KCADSNPRGVSAVLSRSPFDLFIKSPITTCIVDLAPSKGTNLTMSRASKPVNHST 180  
 QY 181 RKEKQRNGTLVTSTLPVGTDRWINGETVYQCRVTHPHLPALMSTTKLPKRLAPEVY 240  
 DB 181 RKEKQRNGTLVTSTLPVGTDRWINGETVYQCRVTHPHLPALMSTTKLPKRLAPEVY 240  
 QY 241 MLPSPSEETGTRTVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKDHGTDPSFPL 300  
 DB 241 MLPSPSEETGTRTVCLIRGFYPSISVQWLFNNEEDHTGHHTTRPKDHGTDPSFPL 299  
 QY 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 342  
 DB 301 YSRMLVVKSIWEKGNLVTCRVVHEALPGSRTLEKSLHYSAGN 341

RESULT 3  
 AAB06207  
 ID AAB06207 standard; protein; 345 AA.  
 AC AAB06207;  
 DT 12-SEP-2003 (revised)  
 DT 22-NOV-2000 (first entry)  
 XX  
 DE Immunogenic peptide consisting of opossum CH2, pig CH3 and opossum CH4.  
 XX  
 KM Pig; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
 KM asthma; eczema; immunogenic peptide.  
 XX  
 OS Didelphis virginiana.  
 OS Sus scrofa.  
 OS Chimeric.  
 OS  
 XX WO200025722-A2.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 21-OCT-1999; 99WO-SR001896.  
 XX  
 PR 02-NOV-1998; 98US-0106552P.  
 PR 22-SEP-1999; 99US-00401636.  
 XX  
 PA (RESI-) RESISTENTIA PHARM AB.  
 XX  
 PI Hellman LT;  
 XX  
 DR WPI; 2000-365342/31.  
 XX  
 PT Immunogenic polypeptides useful for preventing the harmful effects of  
 XX immunoglobulin E in mammals.  
 XX



PS Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy  
CC chain constant regions 2 and 4 of the opossum IGE and the heavy chain  
CC constant region 3 from the pig. It was shown to cause a stronger  
CC polyclonal anti-self IGE response than peptides consisting of the same  
CC regions from one mammal. Immunogenic peptides, particularly those  
CC consisting of different heavy chain constant regions, can be used for  
CC vaccination in humans, against bacterial and viral infections and  
CC allergies, such as asthma, fur, pollen and food allergies and eczema.  
CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 345 AA;

Query Match 85.5%; Score 1587.5; DB 3; Length 345;  
Best Local Similarity 84.7%; Pred. No. 8.8e-124;  
Matches 298; Conservative 14; Mismatches 23; Indels 17; Gaps 4;

QY 1 EHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
DB 1 EHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
QY 61 LVDGGEAENLFPYTRPKREGGQTFSLQSEVNIITQGMMSNTYTCVKNHNSIFEDSSR 120  
DB 61 LVDGGEAENLFPYTRPKREGGQTFSLQSEVNIITQGMMSNTYTCVKNHNSIFEDSSR 120  
QY 121 KC-ADSNPRGVSAVLSRSPFDLFRKSPITICLVVDLAPSKGTNLTWSPAS----- 172  
DB 121 RCTASEPREGVSAVLSRSPFDLFRKSPITICLVVDLAPSKGTNLTWSPAS----- 172  
QY 173 --GKVNHSRKRKEKORNGTLTFTSTLPYGTDMIEGETYQCRVTHPHLPALMSTTKL 230  
DB 173 --GKVNHSRKRKEKORNGTLTFTSTLPYGTDMIEGETYQCRVTHPHLPALMSTTKL 230  
QY 180 PGEPVY-----IKQFNGTFSATISTLPVNSDMEGETTYCNVTHPDLKPLRSIKL 233  
DB 180 PGEPVY-----IKQFNGTFSATISTLPVNSDMEGETTYCNVTHPDLKPLRSIKL 233  
QY 231 PKRLAPVEYVLPSPPEETGTRITVTCILRGFPSEISVQWLFNNEEDHTGHTTRPQK 290  
DB 231 PKRLAPVEYVLPSPPEETGTRITVTCILRGFPSEISVQWLFNNEEDHTGHTTRPQK 290  
QY 234 PKRLAPVEYVLPSPPEETGTRITVTCILRGFPSEISVQWLFNNEEDHTGHTTRPQK 293  
DB 234 PKRLAPVEYVLPSPPEETGTRITVTCILRGFPSEISVQWLFNNEEDHTGHTTRPQK 293  
QY 291 DSGTDPSPFLYSRMLVNSKIMWEKMLVTCRVVHEALPGSRTEKSLHYSAGN 342  
DB 291 DSGTDPSPFLYSRMLVNSKIMWEKMLVTCRVVHEALPGSRTEKSLHYSAGN 342  
DB 294 DSGTDPSPFLYSRMLVNSKIMWEKMLVTCRVVHEALPGSRTEKSLHYSAGN 345

#### RESULT 4

AAB03644 ID AAB03644 standard; protein; 341 AA.

AC AAB03644;

DT 22-NOV-2000 (first entry)

DE Opossum IGE heavy chain constant regions 2, 3 and 4.

XX Opossum; immunoglobulin E; IGE; vaccination; infection; allergy; asthma;  
KW eczema; immunogenic peptide.

OS Didelphis virginiana.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

XX (RESI-) RESISTENTIA PHASM AB.

XX Hellman LT;

XX WPI; 2000-365342/31.

PT Immunogenic polypeptides useful for preventing the harmful effects of  
XX immunoglobulin E in mammals.

PS Disclosure; Fig 1; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy  
CC chain constant regions 2, 3 and 4 of the opossum IGE. It was used to  
CC construct a number of immunogenic peptides which consisted of regions of  
CC IGE from different mammals, which appear to cause a stronger polyclonal  
CC anti-self IGE response than peptides consisting of the same regions from  
CC one mammal. Immunogenic peptides, particularly those consisting of  
CC different heavy chain constant regions, can be used for vaccination in  
CC humans, against bacterial and viral infections and allergies, such as  
CC asthma, fur, pollen and food allergies and eczema.

XX Sequence 341 AA;

Query Match 85.4%; Score 1584.5; DB 3; Length 341;  
Best Local Similarity 85.1%; Pred. No. 1.5e-123;  
Matches 291; Conservative 22; Mismatches 28; Indels 1; Gaps 1;

QY 1 EHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
DB 1 EHHHHHTLSLPESGPVTIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60  
QY 61 LVDGGEAENLFPYTRPKREGGQTFSLQSEVNIITQGMMSNTYTCVKNHNSIFEDSSR 120  
DB 61 LVDGGEAENLFPYTRPKREGGQTFSLQSEVNIITQGMMSNTYTCVKNHNSIFEDSSR 120  
QY 121 KCADSNPRGVSAVLSRSPFDLFRKSPITICLVVDLAPSKGTNLTWSPASGKPVNHST 180  
DB 121 KCSDTPREGVSAVLSRSPFDLFRKSPITICLVVDLAPSKGTNLTWSPASGKPVNHST 179  
QY 181 RKEKORNGTLTFTSTLPYGTDMIEGETYQCRVTHPHLPALMSTTKLPGRLAPEYV 240  
DB 181 RKEKORNGTLTFTSTLPYGTDMIEGETYQCRVTHPHLPALMSTTKLPGRLAPEYV 239  
QY 241 MLPSPPEETGTRITVTCILRGFPSEISVQWLFNNEEDHTGHTTRPQKDGTPSPFL 300  
DB 241 MLPSPPEETGTRITVTCILRGFPSEISVQWLFNNEEDHTGHTTRPQKDGTPSPFL 299  
QY 301 YSRMLVNSKIMWEKMLVTCRVVHEALPGSRTEKSLHYSAGN 342  
DB 301 YSRMLVNSKIMWEKMLVTCRVVHEALPGSRTEKSLHYSAGN 341

#### RESULT 5

AAB06206 ID AAB06206 standard; protein; 341 AA.

AC AAB06206;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

DE Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4.

XX Rat; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;  
KW asthma; eczema; immunogenic peptide.

OS Didelphis virginiana.

XX Ratcetus sp.

XX WO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

(RESI-) RESISTENTIA PHARM AB.  
 Hellman LT;  
 WPI, 2000-365342/31.  
 Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.  
 Disclosure, Fig 2, 50pp; English.  
 The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opsonin IGE and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IGE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema.  
 (Updated on 12-SEP-2003 to standardise OS field)  
 Sequence 341 AA;  
 Query Match 84.5%; Score 1568.5; DB 3; Length 341;  
 Best Local Similarity 83.3%; Pred. No. 3.3e-122;  
 Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;  
 1 EFHHHHHTTLLPESGPTTIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTW 60  
 1 EFHHHHHTTLLPESGPTTIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTW 60  
 61 LVGGEAENLPPTTRPRRGGGQFSLQSEVNTIQQGWSNNTYGVHNGSIPEDSR 120  
 61 LVGGEAENLPPTTRPRRGGGQFSLQSEVNTIQQGWSNNTYGVHNGSIPEDSR 120  
 121 KCADSNPGRVSAVSRPSFDLFRKSPPTTICLVADIAPSKGTNLTWSBAGKPNVHST 180  
 121 RCDSDPRGVTITLPPSPDLVYENGPKITCLVLDL-ESEENITVWVERKKSIGSAS 179  
 181 RKEKQKRGTLVSTLVGTRDMEGTQOCRTVHPLRALMRSTTKLPGRLAPEV 240  
 181 RKEKQKRGTLVSTLVGTRDMEGTQOCRTVHPLRALMRSTTKLPGRLAPEV 240  
 180 CRSTGHNAITSISILPVDKMDISEGQOCRDHDFRKYRSTLPGRLAPEV 239  
 241 MLPSPBETGTRITVTCIRGFYSEISVQWLFNNEEDTGHHTTTRPQDGTDSFPL 300  
 240 MLPSPBETGTRITVTCIRGFYSEISVQWLFNNEEDTGHHTTTRPQDGTDSFPL 299  
 301 YSRMLVNSIWEKGNLVTCRVVHEALPGSRFLKSLHYSAGN 342  
 300 YSRMLVNSIWEKGNLVTCRVVHEALPGSRFLKSLHYSAGN 341  
 RESULT 6  
 ABP96587  
 ID ABP96587 standard; protein; 446 AA.  
 AC ABP96587;  
 XX  
 DT 28-MAY-2003 (first entry)  
 XX  
 DE Opsonin IGE heavy chain amino acid sequence SEQ ID NO:32.  
 XX  
 KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
 KW immune response; major histocompatibility complex; MHC; immunogenic;  
 KW anti-allergic; anti-inflammatory; immunosuppressive; vasoactive; cytostatic;  
 KW dermatological; anti-inflammatory; IGE-mediated condition; food allergy;  
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KW urticaria hives.  
 XX  
 OS Monodelphis domestica.  
 XX  
 PN WO2003015716-A2.

XX 27-FEB-2003.  
 PD 08-AUG-2002; 2002WO-US026986.  
 XX 13-AUG-2001; 2001US-0312120P.  
 PR (IGET-) IGE THERAPEUTICS INC.  
 PA Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 PI WPI, 2003-268242/26.  
 PS  
 XX  
 CC The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IGE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IGE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognize at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IGE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,  
 CC vasoactive, dermatological, anti-inflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IGE, and in  
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IGE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 CC  
 XX  
 SQ Sequence 446 AA;  
 Query Match 82.1%; Score 1523.5; DB 6; Length 446;  
 Best Local Similarity 84.7%; Pred. No. 2.6e-118;  
 Matches 283; Conservative 21; Mismatches 29; Indels 1; Gaps 1;  
 9 TSLPESGPTTIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTWLDGQAE 68  
 114 TSLPESGPTTIPPTVKLFHSSCDPRGDAHSTIOLLCVSGSPAKVHTWLDGQAE 173  
 69 NLPPTTRPRRGGGQFSLQSEVNTIQQGWSNNTYGVHNGSIPEDSRKCADSNPR 128  
 174 NLPPTTRPRRGGGQFSLQSEVNTIQQGWSNNTYGVHNGSIPEDSRKCADSNPR 233  
 129 GVSANVSRPSFDLFRKSPPTTICLVADIAPSKGTNLTWSBAGKPNVHSTREKQKN 188  
 234 GVSANVSRPSFDLFRKSPPTTICLVADIAPSKGTNLTWSBAGKPNVHSTREKQKN 292  
 189 GTITVSTLVGTRDMEGTQOCRTVHPLRALMRSTTKLPGRLAPEVYMLPPSPDE 248  
 293 GTITVSTLVGTRDMEGTQOCRTVHPLRALMRSTTKLPGRLAPEVYMLPPSPDE 352  
 249 TGTTRITVTCIRGFYSEISVQWLFNNEEDTGHHTTTRPQDGTDSFPLYSRMLVNS 308  
 353 TGTTRITVTCIRGFYSEISVQWLFNNEEDTGHHTTTRPQDGTDSFPLYSRMLVNS 412  
 309 SIWEKGNLVTCRVVHEALPGSRFLKSLHYSAGN 342

Db 413 STWKGNIWTCRVVHEALPGSRITLKSJLHYSAGN 446

RESULT 7  
AAB06202

ID AAB06202 standard; protein; 341 AA.

XX AAB06202;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, mouse CH3 and opossum CH4.

XX Mouse; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
XX asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

XX Mus sp.

XX Chimeric.

XX Key Location/Qualifiers  
FT Misc-difference 1..341  
FT /label= OTHER  
FT /note= "Xaa=unknown"

XX MO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX MPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of  
XX immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy  
 XX chain constant regions 2 and 4 of the opossum IgE and the heavy chain  
 XX constant region 3 from the mouse. It was shown to cause a stronger  
 XX polyclonal anti-self IgE response than peptides consisting of the same  
 XX regions from one mammal. Immunogenic peptides, particularly those  
 XX consisting of different heavy chain constant regions, can be used for  
 XX vaccination in humans, against bacterial and viral infections and  
 XX allergies, such as asthma, fur, pollen and food allergies and eczema.  
 XX (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 341 AA;

Query Match 75.0%; Score 1392.5; DB 3; Length 341;

Best Local Similarity 76.7%; Pred. No. 1.5e-107;

Matches 263; Conservative 22; Mismatches 53; Indels 5; Gaps 3;

QY 1 EPHHHHHHTLSLPSGGPTTTPPYKLFHSCDRGDASHITQLCLVSGSPAKVHTW 60

Db 1 EPHHHHHHTLSLPSGGPTTTPPYKLFHSCDRGDASHITQLCLVSGSPAKVHTW 60

QY 61 LVDGGEAENLFPYTRPRGEGGTFSLQSEVNTIQGQWMSNTYTCVKNNGSIFEDSSR 120

Db 61 LVDGGEAENLFPYTRPRGEGGTFSLQSEVNTIQGQWMSNTYTCVKNNGSIFEDSSR 120

QY 121 KCADSNPFGSAVYSRSPFDFLTKRSPTTCLVVDLAPSKGVNLWTSASGKPVNHT 180

Db 121 RCPHPRGVITVYIPSPFLDYOHGAPKLTCLVLDLESEK-HINVTWNGS--KPTXXA 177

Db

QY 181 RK--BEKORNGTLVSTLPVGRDMEIGETVQCRVTHPHLPALMRSTTKLPGKRLADE 238

Db 178 XQWYTHHHHATITXISILPVAKQWIEGYXQIXDHPRIKXVPSITRLPGKRLAX 237

QY 239 VYMLPPSPERTGTTRTVTCILIRGFYPSSEISVQMLFNNEEDHTGHHTTRPOKDHGTDPSF 298

Db 238 VYMLPPSPERTGTTRTVTCILIRGFYPSSEISVQMLFPXEDHTGHHTTRPOKDHGTDPSF 297

QY 299 FLYSRMLVNSKSTWKGNIWTCRVVHEALPGSRITLKSJLHYSAG 341

Db 298 FLYSRMLVNSKSTWKGNIWTCRVVHEALPGSRITLKSJLHYSAG 340

RESULT 8  
AAB06201

ID AAB06201 standard; protein; 342 AA.

XX AAB06201;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, CH4 and rat/opossum CH3.  
XX Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;  
XX asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

XX Rattus sp.

XX Chimeric.

XX Key Location/Qualifiers  
FT Misc-difference 1..342  
FT /label= OTHER  
FT /note= "Xaa=unknown"

XX MO200025722-A2.

XX 11-MAY-2000.

XX 21-OCT-1999; 99WO-SE001896.

XX 02-NOV-1998; 98US-0106652P.

XX 22-SEP-1999; 99US-00401636.

XX (RESI-) RESISTENTIA PHARM AB.

XX Hellman LT;

XX MPI; 2000-365342/31.

XX Immunogenic polypeptides useful for preventing the harmful effects of  
XX immunoglobulin E in mammals.

XX Disclosure; Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy  
 XX chain constant regions 2 and 4 of the opossum IgE and the heavy chain  
 XX constant region 3 created from a combination of the one from the rat and  
 XX the one from the opossum. It was shown to cause a stronger polyclonal  
 XX anti-self IgE response than peptides consisting of the same regions from  
 XX one mammal. Immunogenic peptides, particularly those consisting of  
 XX different heavy chain constant regions, can be used for vaccination in  
 XX humans, against bacterial and viral infections and allergies, such as  
 XX asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-  
 XX 2003 to standardise OS field)

XX Sequence 342 AA;

Query Match 74.1%; Score 1375; DB 3; Length 342;

Best Local Similarity 76.6%; Pred. No. 4.4e-106;  
Matches 262; Conservative 23; Mismatches 55; Indels 2; Gaps 2;

CC 1 EFNHHHTLSLPSGPGVTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 60  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognize at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC Igs peptides, C1-3 have anti-allergic, antiaesthetic, immunosuppressive,  
 CC vasoatropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against Igs, and in  
 CC vaccines. C1-3 are useful for modulating an Igs-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an Igs-mediated condition such as  
 CC Igs-mediated atopic hypersensitivity condition, Igs-mediated non-atopic  
 CC hypersensitivity condition, Igs myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an Igs heavy chain amino acid  
 CC sequence, which is given in an example from the present invention

CC Sequence 427 AA:

Query Match 69.3%; Score 1285.5; DB 6; Length 427;  
 Best Local Similarity 69.6%; Pred. No. 1.7e-98;  
 Matches 234; Conservative 47; Mismatches 52; Indels 3; Gaps 2;

CC 1 EFNHHHTLSLPSGPGVTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 60  
 CC 1 EFNHHHTLSLPSGPGVTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTM 60  
 CC 61 EVDGGEAENLFPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKNKNSIFEDSSR 120  
 CC 61 EVDGGEAENLFPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKNKNSIFEDSSR 120  
 CC 121 KCADNPRGVSAVSRSPFDLFRKSPFTICLVADLAPSKGVTNLWTSRASKPVNHSR 180  
 CC 121 KCADNPRGVSAVSRSPFDLFRKSPFTICLVADLAPSKGVTNLWTSRASKPVNHSR 180  
 CC 121 RQSDDEPRGVITVLLPSPDLVYHGPYKMLCLLD-EESEHIXVWVXERPKXIGXAR 179  
 CC 181 RREKQR-NGLLTVSTPVGTRDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 239  
 CC 181 RREKQR-NGLLTVSTPVGTRDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRY 239  
 CC 180 SLVVEKXHGFTKXSHLPVETDMDIBKTYTXLSESPDMVILPITSLPGRALAPRY 239  
 CC 240 YMLPSPSPERTGTRVTVCLINGFIPSEISVQWLFNNEEDTGHHTTRPOKHGTDPSFP 299  
 CC 240 YMLPSPSPERTGTRVTVCLINGFIPSEISVQWLFNNEEDTGHHTTRPOKHGTDPSFP 299  
 CC 240 YMLPSPSPERTGTRVTVCLINGFIPSEISVQWLFNNEEDTGHHTTRPOKHGTDPSFP 299

CC 300 IYSRMLVNSKIWEKGNLTVCRVHEALPGSRTLEKSLHYAG 341  
 CC 300 IYSRMLVNSKIWEKGNLTVCRVHEALPGSRTLEKSLHYAG 341  
 CC 300 IYSRMLVNSKIWEKGNLTVCRVHEALPGSRTLEKSLHYAG 341

CC RESULT 9  
 CC ABP96591  
 CC ID ABP96591 standard; protein; 427 AA.  
 CC XX  
 CC ABP96591;  
 CC DT 28-MAY-2003 (first entry)  
 CC XX  
 CC DE Brushcail possum Igs heavy chain amino acid sequence SEQ ID NO:36.  
 CC XX  
 CC KW Immunoglobulin E; vaccine; Igs; cytotoxic T lymphocyte response;  
 CC KW immune response; major histocompatibility complex; MHC; immunogenic;  
 CC KW antiallergic; antiaesthetic; immunosuppressive; vasoatropic; cytostatic;  
 CC KW dermatological; antiinflammatory; Igs-mediated condition; food allergy;  
 CC KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 CC KW urticaria hives.  
 CC XX  
 CC OS Trichosurus vulpecula.  
 CC XX  
 CC PN WO2003015716-A2.  
 CC XX  
 CC PD 27-FEB-2003.  
 CC XX  
 CC PF 08-AUG-2002; 2002MO-US026986.  
 CC XX  
 CC PR 13-AUG-2001; 2001US-0312120P.  
 CC XX  
 CC PA (IGET-) IGE THERAPEUTICS INC.  
 CC XX  
 CC PI Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 CC XX  
 CC DR MPI; 2003-268242/26.  
 CC XX  
 CC PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 CC PT against Igs, by identifying peptide eliciting CTL response to Igs  
 CC PT peptides naturally presented by major histocompatibility complex class I  
 CC PT protein.  
 CC XX  
 CC PS Example 7; Page 172-174, 187pp; English.  
 CC XX  
 CC CC The present invention describes a method (M1) for identifying peptides  
 CC CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC CC E (Igs), comprising providing a test peptide (I) suspected of being able  
 CC CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC CC evaluating (I) for ability to elicit in a mammal a CTL response to  
 CC CC naturally processed and presented Igs peptides, where a peptide that

CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognize at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC Igs peptides, C1-3 have anti-allergic, antiaesthetic, immunosuppressive,  
 CC vasoatropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against Igs, and in  
 CC vaccines. C1-3 are useful for modulating an Igs-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an Igs-mediated condition such as  
 CC Igs-mediated atopic hypersensitivity condition, Igs-mediated non-atopic  
 CC hypersensitivity condition, Igs myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an Igs heavy chain amino acid  
 CC sequence, which is given in an example from the present invention

CC Sequence 427 AA:

Query Match 69.3%; Score 1285.5; DB 6; Length 427;  
 Best Local Similarity 69.6%; Pred. No. 1.7e-98;  
 Matches 234; Conservative 47; Mismatches 52; Indels 3; Gaps 2;

CC 7 HHTLSLPSGPGVTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTMVDGQE 66  
 CC 7 HHTLSLPSGPGVTIIIPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTMVDGQE 66  
 CC 95 HVSTGPTKNGPV--IPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTMVDGQE 152  
 CC 95 HVSTGPTKNGPV--IPPTVKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTMVDGQE 152  
 CC 67 AENLFPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKNKNSIFEDSSRCKADSN 126  
 CC 67 AENLFPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKNKNSIFEDSSRCKADSN 126  
 CC 153 AENLFPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKNKNSIFEDSSRCKADSN 212  
 CC 153 AENLFPYTRPRREGGQFSLQSEVNITQGMWSSNTYTCVKNKNSIFEDSSRCKADSN 212  
 CC 127 PRGVSAVLSRSPFDLFRKSPFTICLVADLAPSKGVTNLWTSRASKPVNHSRKEBKQ 186  
 CC 127 PRGVSAVLSRSPFDLFRKSPFTICLVADLAPSKGVTNLWTSRASKPVNHSRKEBKQ 186  
 CC 213 PRGISATLSPSPAFDLYSKAPVLTCLVVDLA-SAEKNVKSWSRSGGTVPSPSVVKEQ 271  
 CC 213 PRGISATLSPSPAFDLYSKAPVLTCLVVDLA-SAEKNVKSWSRSGGTVPSPSVVKEQ 271  
 CC 187 RNLGLVTSITLPGTDMWIEGETYQCVTHPHPALMRSTTLPGKRLAPRYVWVLPSP 246  
 CC 187 RNLGLVTSITLPGTDMWIEGETYQCVTHPHPALMRSTTLPGKRLAPRYVWVLPSP 246  
 CC 272 YNGVITVITSLPQTDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRYVWVLPSP 331  
 CC 272 YNGVITVITSLPQTDWIEGETYQCVTHPHPALMRSTTLPGKRLAPRYVWVLPSP 331  
 CC 247 EFGTTRVTVCLINGFIPSEISVQWLFNNEEDTGHHTTRPOKHGTDPSFPYSRMLV 306  
 CC 247 EFGTTRVTVCLINGFIPSEISVQWLFNNEEDTGHHTTRPOKHGTDPSFPYSRMLV 306  
 CC 332 EERKNTVSLTCLIRAYPADIVVOWLRDKDHTGHHTTRPHKHGDPSPFYSRMVV 391  
 CC 332 EERKNTVSLTCLIRAYPADIVVOWLRDKDHTGHHTTRPHKHGDPSPFYSRMVV 391  
 CC 307 NKSIMKGNLTVCRVHEALPGSRTLEKSLHYAGN 342  
 CC 307 NKSIMKGNLTVCRVHEALPGSRTLEKSLHYAGN 342  
 CC 392 NRSHMOGHTFCRVVHEALPGRTLDKSLHYSTGN 427  
 CC 392 NRSHMOGHTFCRVVHEALPGRTLDKSLHYSTGN 427

CC RESULT 10  
 CC AA019668  
 CC ID AA019668 standard; protein; 569 AA.  
 CC XX  
 CC AC AA019668;  
 CC XX  
 CC DT 28-MAR-2003 (first entry)  
 CC XX  
 CC DE G22 fusion protein for use in treating immune diseases.  
 CC XX  
 CC KW Human; Igs; immunoglobulin E; immunotherapy; immune disease;  
 CC KW Fc receptor; autoimmune disease; constant region; heavy chain;  
 CC KW antiaesthetic; antiallergic; antiinflammatory; dermatological; G22;  
 CC KW antiaesthetic; antineumatic; antidiabetic; neuroprotective;  
 CC KW fusion protein.  
 CC XX  
 CC OS Synthetic.  
 CC XX  
 CC UN Undifferentiated.  
 CC XX  
 CC PN WO200286317-A2.  
 CC XX  
 CC PD 07-NOV-2002.  
 CC XX

Pf	01-MAY--2002; 2002WO-US013527.
Xx	
Pr	01-MAY-2001; 2001US-00847208-
Xx	
Pr	24-OCT-2001; 2001US-00000439.
Xx	
Pa	(REGC ) UNIV CALIFORNIA.
Pt	Saxon A, Zhang K, Zhu D;
Dr	WPI, 2003-103456/09.
Xx	
Pt	New fusion molecules comprising polypeptide sequences that bind to IgG
Ft	inhibitory receptor and native IgE receptor useful for treating IgE-
Pt	mediated hypersensitivity reactions, e.g. asthma or allergies, or
Xx	autoimmune diseases.
Ps	Claim 35; Fig 7; 116pp; English.
Xx	
Cc	The present invention relates to a fusion molecule comprising a first
Cc	polypeptide sequence capable of specific binding to a native IgG
Cc	inhibitory receptor consisting of an immune receptor tyrosine-based
Cc	inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
Cc	functionally connected to a second polypeptide sequence capable of
Cc	specific binding directly or indirectly to a native IgE receptor
Cc	(Fc $\epsilon$ p130n). Also provided are nucleotide sequences encoding such a
Cc	fusion protein. The fusion molecules and compositions are useful for
Cc	treating an IgE-mediated biological response, preferably an IgE-mediated
Cc	hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
Cc	dermatitis, severe food allergies, chronic urticaria, angioedema or
Cc	anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
Cc	type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
Cc	or symptoms resulting from, a type I hypersensitivity reaction in a
Cc	subject receiving immunotherapy. The present sequence is a gammahinge-
Cc	CHgamma2-CHgamma3-(G4ser)3-Chepsilon2-Chepsilon3-Chepsilon3 fusion
Cc	protein (designated GE2) of the invention
Xx	
Sq	Sequence 569 AA;
	Query Match 56.3%; Score 1045.5; DB 6; Length 569;
	Best Local Similarity 58.0%; Pred. No. 2.3e-78;
	Matches 206; Conservative 45; Mismatches 83; Indels 21; Gaps 5;
Qy	3 HHHHHTSLP-----ESGPVITIPPTVLPHSSCPDRGDASTIQLCLV 48
Db	219 NHYQORSLSLSPKAYEGGGSGCGGGSTFPVTVALIQS CDGGHPFTIOLCLV 278
Qy	49 SGSPAKYATWLVDGEALENLFPTTPPKBGGQTFSLOSEVNITGQOMSSNTTYCHV 108
Db	279 SGYPFGTINIWLEDDGYMD-VDLSTLSTTOEGELASTOSHLTSQHWMLSDRYTCOV 336
Qy	109 KHNSIFEDSSRRCKADSNPRGSAYLSRPPDLEFIRKSPFTTCLVLDLASKGTVMLTW 168
Db	337 TYGHTEFDSTRKKCDNSNPGVSATLSRPSPDFLRKSPTTICLVLDLASKGTVMLTW 396
Qy	169 SRAGSKPVNSTRKEEKQRNGTLITYTSLPLVGTRDMIGETIYOQCVTHPHLPALMRSTT 228
Db	397 SRAAGKPVNHSRKRKEKQRNGTLITYTSLPLVGTRDMIGETIYOQCVTHPHLPALMRSTT 456
Qy	229 KLPGKRLAPEYVMLPSPPEETGT--TRTVTCLIRGFYSBSIYQVLPFNNEHDGHHTTT 286
Db	457 KTSGRAPAPERYAFAATPEWPGRNRKRTLACLIOFMEDISVQMHNHEVOLDPRARSTT 515
Qy	287 RPQCDHGTDPSFFLYSRMLVANKSIWEKNLVCVRVHEALPGSRKTLEKSLHYSAG 341
Db	516 QPKTKGS-GPFVFSRLVEVTRAWEQKDFICRAVHAASPSQTVORAHSVNPQ 568
	RESULT 11
ID	ABP96584
XX	ABP96584 standard; protein; 577 AA.
XX	ABP96584;

28-MAY-2003 (first entry)  
Duckbilled platypus IGE heavy chain amino acid sequence SEQ ID NO:29.  
Immunoglobulin B; vaccine; IGE; cytotoxic T lymphocyte response;  
immune response; major histocompatibility complex; MHC; immunogenic;  
antiallergic; antiallergic; immunosuppressive; vasotropic; cytotoxic;  
dermatological; antinflammatory; IGE-mediated condition; food allergy;  
atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
urticaria hives.  
Ornithorhynchus anatinus.  
WO2003015716-A2.  
27-FEB-2003.  
08-AUG-2002; 2002WO-US026986.  
13-AUG-2001; 2001US-0312120P.  
(IGET-) IGE THERAPEUTICS INC.  
Chen SA, Yang Y, Barankiewicz T, Chen Z;  
WPI, 2003-268242/26.  
Example 7: Page 154-157, 187pp; English.  
The present invention describes a method (M1) for identifying peptides  
that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
B (IGE), comprising providing a test peptide (T) suspected of being able  
to bind to major histocompatibility complex (MHC) class I molecule, and  
evaluating (T) for ability to elicit in a mammal a CTL response to  
naturally processed and presented IGE peptides, where a peptide that  
induces such a response is identified. Also described are compositions:  
(C1) comprising at least one immunogenic peptide (I) identified by (M1);  
(C2) comprising at least one isolated polynucleotide encoding (I); and  
(C3) comprising antigen-presenting cells that recognise at least one (I).  
Where C1-3 are able to bind to at least one MHC class I molecule and to  
elicit in a mammal a CTL response to naturally processed and presented  
IGE peptides. C1-3 have antiallergic, antiallergic, immunosuppressive,  
vasotropic, dermatological, antinflammatory and cytotoxic activities,  
and can be used as inducers of a CTL response against IGE, and in  
vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
useful for treating atopic hypersensitivity conditions (such as allergic  
rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
hives). The present sequence represents an IGE heavy chain amino acid  
sequence, which is given in an example from the present invention  
Sequence 577 AA;  
Query Match 56.2%; Score 1044; DB 6; Length 577;  
Best Local Similarity 57.4%; Pred. No. 3.2e-78;  
Matches 187; Conservative 63; Mismatches 70; Indels 6; Gaps 4;  
21 IIPVYKLFHSSCDPRGASHSTIOLCLVSGSPAKVHYTMLVDOGBANLTPYTRPRE 80  
254 IIPVYKLFHSSCDPRGASHSTIOLCLVSGSPAKVHYTMLVDOGBANLTPYTRPRE 313  
81 GGQTFSSQSEVNIITGQGMSSNTYTCVKH--NCSIFEDSSRKCADSNFRVSAVLSRPS 138  
314 GNRFFSSHSSEVNIITGQGMSSNTYTCVKH--NCSIFEDSSRKCADSNFRVSAVLSRPS 373

QY 139 PFDLFRKSPITTCVVDLAPSKGTVNTWGRASGKPVNSTRKEKQKNGTLTVSTLP 198  
 DB 374 PFDLYISKTKPLTCLIIDVSTEG--MEVWRSRSTPLASPEEQKNGTMSFISTVP 432  
 QY 199 VGRDRIEGETYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPSPPEET--GTRIVY 256  
 DB 433 VNIQDNESGTYTCVAHDLPSPIKIVTKLPKRLAPEVYAPFPQGAVSQDSLSLT 492  
 QY 257 CLIRGYTPEISVQVLPNNEEDHTGHTTTPQKHGDPSEFLYSRLVNSIWEKGNL 316  
 DB 493 CLIRGYTPEISVRLNKLPTREHYTKTKPLKQDGPFAFLYSRLVNSIWEKGNV 552  
 QY 317 VTCRVVHEALPGSRTEKSLHYSAGN 342  
 DB 553 YTCQVHHEALP--SRNTERKFGHTSGN 577

RESULT 12  
 ID AA019667 standard; protein; 320 AA.  
 AC AA019667;  
 XX  
 DT 28-MAR-2003 (first entry)  
 DE Human IgE heavy chain constant region CH2-CH3-CH4 portion.  
 XX  
 KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;  
 KW Fcεp10n receptor; autoimmune disease; constant region; heavy chain;  
 KW antisthmatic; antiallergic; antiinflammatory; dermatologic;  
 KW antihistaminic; antineumatic; antidiabetic; neuroprotective;  
 KW CH2-CH3-CH4 region.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200288317-A2.  
 XX  
 PD 07-NOV-2002.  
 XX  
 PF 01-MAY-2002; 2002WO-US013527.  
 XX  
 PR 01-MAY-2001; 2001US-00847208.  
 XX  
 PR 24-OCT-2001; 2001US-00000439.  
 XX  
 PA (REGC) UNIV CALIFORNIA.  
 XX  
 PI Saxon A, Zhang K, Zhu D;  
 XX  
 DR WPI; 2003-103456/09.  
 XX  
 PT New fusion molecules comprising polypeptide sequences that bind to IgE  
 PT inhibitory receptor and native IgE receptor, useful for treating IgE-  
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
 PT autoimmune diseases.  
 XX  
 PS Claim 21; Fig 6; 116pp; English.  
 XX  
 CC The present invention relates to a fusion molecule comprising a first  
 CC polypeptide sequence capable of specific binding to a native IgE  
 CC inhibitory receptor consisting of an immune receptor tyrosine-based  
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
 CC functionally connected to a second polypeptide sequence capable of  
 CC specific binding directly or indirectly to a native IgE receptor  
 CC (Fcεp10n). Also provided are nucleotide sequences encoding such a  
 CC fusion protein. The fusion molecules and compositions are useful for  
 CC treating an IgE-mediated biological response, preferably an IgE-mediated  
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,  
 CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgE

CC heavy chain constant region CH2-CH3-CH4 portion  
 XX  
 SQ Sequence 320 AA;  
 Query Match 56.0%; Score 1038.5; DB 6; Length 320;  
 Best Local Similarity 62.4%; Pred. No. 4.3e-78;  
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTKTLFHSQCDPRGDAHSTTQLCLVSGSPAKAHVTLVDQDAENLPYTRPKKSG 81  
 DB 3 PPYKTLIQSSCDGGRFPPTIQLCLVSGYTPGTINITWLEDQVWD--VDLSTASTQE 60  
 QY 82 GQFSLQSEVNIQGGWMSNTYTCVKNNGSIFEDSSKCKADSNPRGVSAVLSPPSPD 141  
 DB 61 GELASTQSELTLEQKMLSDRTTCQVYQGHTEFSTKCKADSNPRGSAVLSPPSPD 120  
 QY 142 LFIKSPITTCVVDLAPSKGTVNTWGRASGKPVNSTRKEKQKNGTLTVSTLPVGT 201  
 DB 121 LFIKSPITTCVVDLAPSKGTVNTWGRASGKPVNSTRKEKQKNGTLTVSTLPVGT 180  
 QY 202 RDMIEGETYQCRVTHPLPALMRSTTKLPGKRLAPEVYMLPSPPEET--TRIVTCL 259  
 DB 161 RDMIEGETYQCRVTHPLPALMRSTTKSGRAAPEVYAP--ATPEWGSRDKRTLACLI 239  
 QY 260 RGFYPSISVQVLPNNEEDHTGHTTTPQKHGDPSEFLYSRLVNSIWEKGNLYTC 319  
 DB 240 QNFPEEDISVQVWLNHEVQLPDARHSTTOPRKTKGS--GFVFSRLVTRAEWQKDEFTC 297  
 QY 320 RVVHEALPGSRTEKSLHYSAGN 341  
 DB 298 RAVHEALSPQGTQRAVSVNVP 319

RESULT 13  
 ID AA080286 standard; protein; 323 AA.  
 AC AA080286;  
 XX  
 DT 30-JUL-2002 (first entry)  
 DE Human IgE C2-C3-C4 domains for E. Coli expression.  
 XX  
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
 KW antisthmatic; dermatologic; antiinflammatory; immunoglobulin E; IgE;  
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
 KW heavy chain C domain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN Synthetic.  
 XX  
 PN WO200220038-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 06-SEP-2001; 2001WO-DK000579.  
 XX  
 PR 06-SEP-2000; 2000DK-00003326.  
 XX  
 PR 15-SEP-2000; 2000US-0232831P.  
 XX  
 PA (PHAR-) PHARMEXA AS.  
 XX  
 PI Klyener S, Von Hoegen P, Voldborg B, Gautam A;  
 XX  
 DR WPI; 2002-383033/41.  
 XX  
 DR N-PSDB; ABK51134.  
 XX  
 PT Inducing immune response against autologous immunoglobulin E in an  
 PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
 PT epitope an/or B-cell epitope derived from the immunoglobulin.  
 XX  
 PS Disclosure; Page 112-113; 151pp; English.  
 XX

CC This invention relates to a novel method for inducing an immune response  
 CC against autologous immunoglobulin E (IgE) in an animal. The method  
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell  
 CC epitope (TH epitope) which is foreign to the animal, by antigen  
 CC presenting cells (APCs) of the animal's immune system. The epitopes of  
 CC the invention may be used as a vaccine against allergic diseases. The  
 CC method of the invention is useful for inducing an immune response against  
 CC autologous IgE in an animal, which is useful for downregulating  
 CC autologous IgE in the animal. This method is useful in the prevention and  
 CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
 CC asthma and atopic dermatitis. The present sequence represents the human  
 CC IgE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli  
 CC system, this sequence was used to create the epitopes of the invention  
 XX  
 SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;  
 Best Local Similarity 62.4%; Pred. No. 4.3e-78;  
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVGQEAENLFYTRPRKRG 81  
 DB 6 PPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLBQVMD--VDLSTASTQGE 63  
 QY 82 GQTFSLQSEVNTTQGMMSNTYTCVYKNGSIFEDSSRKCADSNPRGVSAVLSRPSFPD 141  
 DB 64 GELASTQSELTLSQKHWLSDRTYTCQVYVQGHTEFDSYRKCADSNPRGVSAVLSRPSFPD 123  
 QY 142 LFIKSPFTTCLVVDLAPSKGTVNLTWGRASGKPVNHSRTRKEKORNGTLVTSILPVG 201  
 DB 124 LFIKSPFTTCLVVDLAPSKGTVNLTWGRASGKPVNHSRTRKEKORNGTLVTSILPVG 183  
 QY 202 RDMWIGETVQCRVTHPHLPALMRSTTKLPGKRLAPBYVYMLPSPDETGT--TRTVTGLI 259  
 DB 184 RDMWIGETVQCRVTHPHLPALMRSTTKLPGKRLAPBYVYMLPSPDETGT--TRTVTGLI 242  
 QY 260 RGFYSEISVQWLFNNEBDHGTHTTRPOKHGDPSPFLYSRNLVNSIWEKGNLVTG 319  
 DB 243 QNFMEEDISVQWLNHEVQLPDARHSTTOPKRTKGS--GFVFSRLVTRAEWQKDEFTIC 300  
 QY 320 RVVHEALPGSRTLEKSLHYSG 341  
 DB 301 RAVHEAASPSQTVQRAVSVNPG 322

## RESULT 14

AAU80285  
 ID AAU80285 standard; protein; 323 AA.

AC AAU80285;  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Human IgE C2-C3-C4 domains for mammalian expression.  
 XX  
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;  
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
 KW heavy chain C domain.

OS Homo sapiens.  
 OS Synthetic.

XX WO200220038-A2.

XX 14-MAR-2002.

XX 06-SEP-2001; 2001WO-DK000579.

XX 06-SEP-2000; 2000DK-0000136.  
 XX 15-SEP-2000; 2000US-0232831P.

PA (PHAR-) PHARMEXA AS.

XX Klyser S, Von Hoegen P, Voldborg B, Gautam A;

XX WPT, 2002-383033/41.

XX N-PSDB; ABR51133.

PT Inducing immune response against autologous immunoglobulin E in an  
 PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte  
 PT epitope and/or B-cell epitope derived from the immunoglobulin.

PS Disclosure, Page 108-110; 151pp; English.

XX  
 XX  
 CC This invention relates to a novel method for inducing an immune response  
 CC against autologous immunoglobulin E (IgE) in an animal. The method  
 CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte  
 CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell  
 CC epitope (TH epitope) which is foreign to the animal, by antigen  
 CC presenting cells (APCs) of the animal's immune system. The epitopes of  
 CC the invention may be used as a vaccine against allergic diseases. The  
 CC method of the invention is useful for inducing an immune response against  
 CC autologous IgE in an animal, which is useful for downregulating  
 CC autologous IgE in the animal. This method is useful in the prevention and  
 CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,  
 CC asthma and atopic dermatitis. The present sequence represents the human  
 CC IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian  
 CC system, this sequence was used to create the epitopes of the invention  
 XX  
 SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;  
 Best Local Similarity 62.4%; Pred. No. 4.3e-78;  
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;

QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTWLVGQEAENLFYTRPRKRG 81  
 DB 6 PPTVKILQSSCDGGHFPPTIQLCLVSGYTPGTINITWLBQVMD--VDLSTASTQGE 63  
 QY 82 GQTFSLQSEVNTTQGMMSNTYTCVYKNGSIFEDSSRKCADSNPRGVSAVLSRPSFPD 141  
 DB 64 GELASTQSELTLSQKHWLSDRTYTCQVYVQGHTEFDSYRKCADSNPRGVSAVLSRPSFPD 123  
 QY 142 LFIKSPFTTCLVVDLAPSKGTVNLTWGRASGKPVNHSRTRKEKORNGTLVTSILPVG 201  
 DB 124 LFIKSPFTTCLVVDLAPSKGTVNLTWGRASGKPVNHSRTRKEKORNGTLVTSILPVG 183  
 QY 202 RDMWIGETVQCRVTHPHLPALMRSTTKLPGKRLAPBYVYMLPSPDETGT--TRTVTGLI 259  
 DB 184 RDMWIGETVQCRVTHPHLPALMRSTTKLPGKRLAPBYVYMLPSPDETGT--TRTVTGLI 242  
 QY 260 RGFYSEISVQWLFNNEBDHGTHTTRPOKHGDPSPFLYSRNLVNSIWEKGNLVTG 319  
 DB 243 QNFMEEDISVQWLNHEVQLPDARHSTTOPKRTKGS--GFVFSRLVTRAEWQKDEFTIC 300  
 QY 320 RVVHEALPGSRTLEKSLHYSG 341  
 DB 301 RAVHEAASPSQTVQRAVSVNPG 322

## RESULT 15

AAU80284  
 ID AAU80284 standard; protein; 323 AA.

AC AAU80284;  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Human IgE heavy chain C2-C3-C4 domains.  
 XX  
 KW IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;  
 KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;  
 KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;  
 KW heavy chain C domain.







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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:57:11 ; Search time 45 Seconds

(without alignments)  
2397.938 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EPHHHHHHTSLPESGPVTI.....HEALPGSRITLKSIIHYSAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	482.5	26.0	337	6 Q95M34	Q95M34 equus caball
2	479.5	25.8	473	4 Q8TC63	Q8TC63 homo sapien
3	470	25.3	614	11 Q7TMT6	Q7TMT6 mus musculu
4	469	25.3	613	11 Q8VCX7	Q8VCX7 mus musculu
5	465	25.1	375	4 Q86T11	Q86T11 homo sapien
6	465	25.1	588	4 Q8WUX4	Q8WUX4 homo sapien
7	465	25.1	597	4 Q8BUI0	Q8BUI0 homo sapien
8	465	25.1	597	4 Q8BQB8	Q8BQB8 homo sapien
9	465	25.1	597	4 Q8BQB9	Q8BQB9 homo sapien
10	465	25.1	613	4 Q8WUX1	Q8WUX1 homo sapien
11	465	25.1	613	4 Q8WUX1	Q8WUX1 homo sapien
12	465	25.1	614	4 Q8WUX1	Q8WUX1 homo sapien
13	465	25.1	618	4 Q8WUX1	Q8WUX1 homo sapien
14	465	25.1	618	4 Q8WUX1	Q8WUX1 homo sapien
15	465	25.1	618	4 Q8WUX1	Q8WUX1 homo sapien
16	465	25.1	618	4 Q8WUX1	Q8WUX1 homo sapien

17	446	24.0	521	4 Q8N4Y9	Q8N4Y9 homo sapien
18	444	23.9	509	4 Q8N4Y7	Q8N4Y7 homo sapien
19	441	23.8	354	4 Q86T12	Q86T12 mus musculu
20	440.5	23.7	437	11 Q9R1A4	Q9R1A4 mus musculu
21	440	23.7	463	11 Q9R1C4	Q9R1C4 mus musculu
22	440	23.7	469	11 Q8R3V9	Q8R3V9 mus musculu
23	421	22.7	473	11 Q8R3V9	Q8R3V9 mus musculu
24	402.5	21.7	679	4 Q8R3V9	Q8R3V9 mus musculu
25	399	21.5	468	11 Q9R1J1	Q9R1J1 mus musculu
26	399	21.5	473	11 Q9R1J1	Q9R1J1 mus musculu
27	398	21.4	470	11 Q7TMT1	Q7TMT1 mus musculu
28	395.5	21.3	473	11 Q9R1J1	Q9R1J1 mus musculu
29	395.5	21.3	474	11 Q8R3H6	Q8R3H6 mus musculu
30	371.5	20.0	492	4 Q7Z374	Q7Z374 homo sapien
31	370.5	20.0	478	4 Q7Z379	Q7Z379 homo sapien
32	369.5	19.9	416	4 Q8NPP6	Q8NPP6 homo sapien
33	360	19.4	493	4 Q8NCT6	Q8NCT6 homo sapien
34	359	19.3	384	4 Q8NPP6	Q8NPP6 homo sapien
35	358	19.3	494	4 Q8NCT6	Q8NCT6 homo sapien
36	358	19.3	496	4 Q8NCT6	Q8NCT6 homo sapien
37	358	19.3	497	4 Q8NCT6	Q8NCT6 homo sapien
38	355.5	19.2	499	4 Q8NCT6	Q8NCT6 homo sapien
39	355.5	19.2	499	4 Q8NCT6	Q8NCT6 homo sapien
40	351.5	18.9	496	4 Q8NCT6	Q8NCT6 homo sapien
41	348	18.8	426	11 Q9DCD9	Q9DCD9 mus musculu
42	346	18.6	500	4 Q8R3V9	Q8R3V9 mus musculu
43	345	18.6	486	11 Q9R1J1	Q9R1J1 mus musculu
44	345	18.6	487	11 Q9R1J1	Q9R1J1 mus musculu
45	338.5	18.2	479	11 Q9R1J1	Q9R1J1 mus musculu

## ALIGNMENTS

RESULT 1  
ID Q95M34 PRELIMINARY: PRT; 337 AA.  
AC Q95M34:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Immunoglobulin gamma 1 heavy chain constant region (Fragment).  
GN IGHCI.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_Taxid=9796;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Wagner B.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98383416; PubMed=9717671;  
RA Wagner B.; Overesch G.; Sheoran A.; Holmes M.; Richards C.;  
RA Leibold W.; Radbruch A.;  
RT "Organization of the equine immunoglobulin heavy chain constant region  
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";  
RL Immunobiology 199;105-119(1998).  
DR EMBL, AJ300675; CAC44624.1;  
DR InterPro, IPR007110; IG\_1like.  
DR InterPro, IPR003597; IG\_C1.  
DR InterPro, IPR003006; IG\_MHC.  
DR Pfam, PF00047; Ig\_2.  
DR SMART, SM00407; IGH1; 2.  
DR PROSITE, PS00835; IG\_LIKE; 3.  
DR PROSITE, PS00290; IG\_MHC; 2.  
FT NON\_TER  
SQ SEQUENCE 337 AA; 37438 MW; A60BFB01DEPDI16 CRC64;  
Query Match 26.0%; Score 482.5; DB 6; Length 337;  
Best Local Similarity 32.8%; Pred. No. 3.9e-36;  
Matches 113; Conservative 67; Mismatches 120; Indels 45; Gaps 12;

QY 23 PTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW----LYDQGEANLFPYTTBP 78  
 DB 6 PVFALADCGCTTSD--STVALGCLVSGYFPEPVKSVNSSLTSG--VHTFSPVL-- 57  
 QY 79 REGGQFSLQSEVNITQCGMSSNTYTCHVKANGSIFE-----DSRRKCADSN--P 127  
 DB 58 -QSSGFYSLSSMVTVPASTM--TSEYIYCNVHAASNFVDRIRIPIDPNQKCDMCKCP 115  
 QY 128 R-----GVSAYISRPSPD-LPIKSPITTCVVDLASKGTVALTMSRAGKCVNH 178  
 DB 116 KCPABELLGGSPVFLFPNPKDTLMTITPEVTCVVVDVSOENPDYKFMWMDGVEVTA 175  
 QY 179 STRKEKORNGTLVYTSITLPVGTDRMIGETVQCVTRPHLPALMRSTTLPGKRLAPE 238  
 DB 176 TTRPEBQPNSTYRVVSVLRIQHOMLSGKEFKCVNNOALPPIERITITTKRSQEPQ 235  
 QY 239 VYMLPSPPEGTTR-TTTCIRGYPSEISVQMLFNNEEDHTGHTTTRPQKHGTDPS 297  
 DB 236 VYVLAHPHDELKSKSVATCVKDYFPEINIMESNQGPELETKYSTTQAOQD--SDGS 293  
 QY 298 FFLYSRMLVYKSIWEKGNLVTGRVYHEALPGSRITLKSLSHYSAGN 342  
 DB 294 VFLYSKLSYDRNMQGGITTCGVNHEALHN-----HTTQKN 330

## RESULT 2

Q8TC63 PRELIMINARY; PRT; 473 AA.  
 ID Q8TC63  
 AC Q8TC63  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Tissue=Kidney;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025985; AAH25985.1; -  
 DR GO; GO:0005507; F-actin binding; IEA.  
 DR GO; GO:0005489; F-actin transport; IEA.  
 DR GO; GO:0006118; P-selectin transport; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig\_1.  
 DR SMART; SM00406; IGV\_1.  
 DR PROSITE; PS00196; COPPER\_BLUE; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 25.8%; Score 479.5; DB 4; Length 473;  
 Best Local Similarity 34.9%; Pred. No. 12e-35;  
 Matches 120; Conservative 62; Mismatches 129; Indels 33; Gaps 11;

QY 18 VTIIPPTVK---LFHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW----LYDQGEANL 70  
 DB 142 VASVPASTKGPSPVFLAPCSRSTSTALGCLVDFPEPYVSWNSGALTSG--VHT 198  
 QY 71 FYYTTRKREGGQFSLQSEVNITQCGMSSNTYTCHVKANGSIFE-----BDSRRKCADSNP--- 127  
 DB 199 FPAVL---QSSGLYSLSSMVTVPSSS-LGITTYICNVDPHPSNTKVDKRVESKYGPECP 253  
 QY 128 -----RGVSAYISRPSPD-LPIKSPITTCVVDLASKGTVALTMSRAGKCVNH 178

DB 254 SCPAPFLGSPVFLFPKPKDTLMTISRTPEVTCVVVDVSOEDPEVQFNWYDVGEVHNA 313  
 QY 179 STRKEKORNGTLVYTSITLPVGTDRMIGETVQCVTRPHLPALMRSTTLPGKRLAPE 238  
 DB 314 KTRPREQNSYRVVSVLTVLHQDLNKEKEKCVSKNGKPSISIEKTSIRKKGQPRBPQ 373  
 QY 239 VYMLPSPPEE-TGTRITVTCIRGYPSEISVQMLFNNEEDHTGHTTTRPQKHGTDPS 297  
 DB 374 VYTLPPSQEHTKNGVSLTCLVKGYFIPSDIAEMESNQGPER--NYKTTPTLD--SDGS 429  
 QY 298 FFLYSRMLVYKSIWEKGNLVTGRVYHEALPGSRITLKSLSHYSAG 341  
 DB 430 FFLYSRLTVDKSRWQGNVFSQVNHKALHNHTT-QXSLSLSLG 472

## RESULT 3

Q7TMT6 PRELIMINARY; PRT; 614 AA.  
 ID Q7TMT6  
 AC Q7TMT6  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
 RX MEDLINE=22386257; PubMed=12477932;  
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;  
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schuler G.D.;  
 RA Altschul S.F.; Zeeberg B.; Buelow K.H.; Scheefter C.F.; Bhat N.K.;  
 RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;  
 RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;  
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;  
 RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carroll P.; Prange C.;  
 RA Raha S.S.; Loggiano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;  
 RA Bosak S.A.; McEwan P.J.; McKernan K.U.; Malek J.A.; Gunaratne P.H.;  
 RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hultk S.W.;  
 RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;  
 RA Fahy J.; Hellon E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;  
 RA Whiting R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;  
 RA Rodriguez A.C.; Gilwood J.; Schmutz J.; Myers R.M.; Butterfield Y.S.;  
 RA Krzywinski M.I.; Skalska U.; Smaltz D.E.; Scherch A.; Schein J.E.;  
 RA Jones S.J.; Matra M.A.;  
 RA "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
 RA Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC053409; AAH53409.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 614 AA; 67746 MW; 839BAF3BD124F89 CRC64;

Query Match 25.3%; Score 470; DB 11; Length 614;  
 Best Local Similarity 34.1%; Pred. No. 1.3e-34;  
 Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;

QY 23 PTVKLFHSSCDPR---GDHSTIQLCLVSGFSPAKVHTWLVNDQGEANLFP---PYTT 75  
 DB 250 PNVNVF---VPPDRGSGAPAPKRSKILCEATNFTPKPIVSWLKGKIVSGFTTDPVTI 306  
 QY 76 RPRREGGQFSLQSEVNITQCGMSSNTYTCHVKANGSIFE-----BDSRRKCADSNPPOVSXVL 134  
 DB 307 ENKGSTPQYKYSTLTITSEIDMLNLYTCVDRGLFLKLVNSTGCAASSTDLIFT 366  
 QY 135 SRPSPDLPIKSPITTCVVDLASKGTVALTMSRAGKCVNHSTRKEKORNGTLTVT 194

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Db      367 IPPSFADITLKSANLTCVSNLATYE-TLNISWASOGSEPLETKIKIMESHNGTSPSAK 425
Qy      195 STLPVGTNRWIGETTYQCRVTHPHLPRALMRSTTLPGK--RLAEVYMLPPSEETG-- 250
Db      426 GVAACVCEDEMNRRKFEVCTVTHRDLPSPQKFKISK-PNEVHGHPPAVYLLPPAREQNLNR 484
Qy      251 TTRTVYCLIRGFYPSISVQWLFNNBEDHTGHTTRPQKHGTDPSFELYRMLVNSKI 310
Db      485 ESATYTCVAKGFSPADISVQWLOQGLLPQEKYVTSAMPBEGAGGFYFTHSILTVBEE 544
Qy      311 WEKGNLVTCRVVHEALP--GSRTLEKS 335
Db      545 WNSGETYTCVSHVHEALPHLVTERTVDKS 572

```

## RESULT 4

```

ID      Q8VCK7      PRELIMINARY;      PRT;      613 AA.
AC      Q8VCK7;
DT      01-MAR-2002 (Tremblrel. 20, Created)
DT      01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT      01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE      Hypothetical protein.
GN      IGH-6.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Salivary gland;
RL      Strauberg R.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC018315; AAL18315.1; -.
DR      MGI; MGI:96448; Igh-6.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003586; IG_v.
DR      Pfam; PF00047; Ig_5.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 5.
DR      PROSITE; PS00290; IG_MHC; 3.
KW      Hypothetical protein.
SQ      SEQUENCE 613 AA; 67855 MW; 41A9384D4C22862 CRC64;

```

Query Match 25.3%; Score 469; DB 11; Length 613;  
 Best Local Similarity 34.1%; Pred. No. 1.6e-34;  
 Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;

```

Qy      23 PTYKLFHSSCDPR---GDAHSTIOLCLVSGSPAKVHTVWLVDGQEAENLF---PYTT 75
Db      249 PAVNVF--VPRDGFSGAPRKSKLICEATNFTPKPTVSNLKGKLVESGFTTDPVTI 305
Qy      76 RKRREGGQTFSLQSEVNTTQGMSSNTYTCVKNGSIF-EDSRKCAADSNPKGSAVL 134
Db      306 ENKSGTPQTYKVISLTLTISEIDMLNLYTCVDRHGLTFLKNVSSSTCAASPTDILFT 365
Qy      135 SRPSFDLPIRKSPTITCLVVDLAPSKGVNLTWGRASGKPVNSTRKEEQNRGLTVT 194
Db      366 ITPSPADITLKSANLTCVSNLATYE-TLNISWASOGSEPLETKIKIMESHNGTSPSAK 424
Qy      195 STLPVGTNRWIGETTYQCRVTHPHLPRALMRSTTLPGK--RLAEVYMLPPSEETG-- 250
Db      425 GVAACVCEDEMNRRKFEVCTVTHRDLPSPQKFKISK-PNEVHGHPPAVYLLPPAREQNLNR 483
Qy      251 TTRTVYCLIRGFYPSISVQWLFNNBEDHTGHTTRPQKHGTDPSFELYRMLVNSKI 310
Db      484 ESATYTCVAKGFSPADISVQWLOQGLLPQEKYVTSAMPBEGAGGFYFTHSILTVBEE 543
Qy      311 WEKGNLVTCRVVHEALP--GSRTLEKS 335
Db      544 WNSGETYTCVSHVHEALPHLVTERTVDKS 571

```

## RESULT 5

```

ID      Q86TT1      PRELIMINARY;      PRT;      375 AA.
AC      Q86TT1;
DT      01-JUN-2003 (Tremblrel. 24, Created)
DT      01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT      01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE      Human full-length cDNA clone C30DD006YL02 of neuroblastoma of Homo
DE      sapiens (Human).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Neuroblastoma;
RA      Genoscope; (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Neuroblastoma;
RA      Li W.B., Gruber C., Jessee J., Polayes D.;
RL      "Full-length cDNA libraries and normalization."
RL      Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BX161420; CAD61894.1; -.
DR      GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR      InterPro; IPR007110; IG_1like.
DR      InterPro; IPR003597; IG_c1.
DR      InterPro; IPR003006; IG_MHC.
DR      Pfam; PF00047; Ig_3.
DR      SMART; SM00407; Igcl; 3.
DR      PROSITE; PS50835; IG_LIKE; 3.
DR      PROSITE; PS00290; IG_MHC; 3.
KW      Plasmid.
SQ      SEQUENCE 375 AA; 41272 MW; 7ACD1AF439C5EFC CRC64;

```

Query Match 25.1%; Score 465; DB 4; Length 375;  
 Best Local Similarity 31.1%; Pred. No. 1.9e-34;  
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

```

Qy      17 PVTII---PVTYVLFHSSCDPR---GDAHSTIOLCLVSGSPAKVHTVWLVDGQEAEN 69
Db      24 PLVIVALEPRKVSF--VPRDGFSGAPRKSKLICEATNFTPKPTVSNLKGKLVESGFTTDPVTI 305
Qy      70 LFPTT-----RKRREGGQTFSLQSEVNTTQGMSSNTYTCVKNGSIF-EDSRKCA 123
Db      80 --GVTDQVQAEKESGPTTYKVTSTLTIKESDMISQSMFTCRVDRHGLTFOQNASMCG 137
Qy      124 DSNPRGSAVLSRPSFDLPIRKSPTITCLVVDLAPSKGVNLTWGRASGKPVNSTRKE 183
Db      138 PDDDTAIRPAIPSPASIFLTKSTKTLCLVVDLT-TYVSVITISWRONGEAVKHTNIS 196
Qy      184 EKQRNGTLVTVSTLPVGTDMWIGETTYQCRVTHPHLPRALMRSTTLPGKRL-APVYML 242
Db      197 ESHPNATFSVAGRASCEBDWNSGERFTCTVHTDLPSELKQTIISPKVLAHRPQVYLL 256
Qy      243 PSPEETG--TTRTVYCLIRGFYPSISVQWLFNNBEDHTGHTTRPQKHGTDPSFL 300
Db      257 PPAREQNLNRSAITTCVAKGFSPADISVQWLOQGLLPQEKYVTSAMPBEGAGGFYFTHS 316
Qy      301 YSHMLVNSKIWEKGNLVTCRVVHEALP--GSRTLEKS 335
Db      317 HSLITVSEEMNTGETYTCVSHVHEALPHLVTERTVDKS 572

```

## RESULT 6

```

ID      Q8WUX4      PRELIMINARY;      PRT;      588 AA.
AC      Q8WUX4;
DT      01-MAR-2002 (Tremblrel. 20, Created)
DT      01-MAR-2002 (Tremblrel. 20, Last sequence update)

```

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019235; AAH19235.1; -  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein  
 SQ SEQUENCE 588 AA; 64438 MW; FCG0DBAD82B39FD7 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 588;  
 Best Local Similarity 31.1%; Pred. No. 3.5e-34;  
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

QY 17 PTITL---PPTVTLFSSCDPR---GDAHSTIQLCLVSGSPAKVHTVTVDQGEAKN 69  
 DB 246 PLPVIAELPPKVSF---VPRDGFEGNPKRS-KLICQATGSPROIOVSWLRGKQVGS 301  
 QY 70 LPEYTT----RPKEGQTFSLQSEVNITQGMSSNTYTCVHGNSIF-EDSRKCA 123  
 DB 302 --GVTTDQVAAKESGPTTYKVTSTLTIKESDWSQSMFCRDVHRGLTFQANASMCV 359  
 QY 124 DSNPRGVSAYLSRSPFPDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNHSRKE 183  
 DB 360 PQDDTAIRVFALPPSPASIFLTGSTLTCLVTDLT-TYDSVTISWTRONGEAVKTHNIS 418  
 QY 184 EKQRNGTLTVSTLTPVGTDMIEGETYQCRVTHPHLPALNRSTTKLPKRL-APEVYML 242  
 DB 419 ESHPNATFSAVGEASICEDDWSGERFTCTVHTDLPSPKQISRPGVALHRPDYLL 478  
 QY 243 PPSPEBTG--TTRVTCLIRGYPSSEISVQMLFNNEDHTGHTTRPQKHGTDPSPFL 300  
 DB 479 PPARQELNRESATITCLVTFSPADVFQVMQRQCPSPKXYTSAPMPPOAGRYFA 538  
 QY 301 YSRMLVNSIWEKGNLVCRVVHEALPG---SRTLEKS 335  
 DB 539 HSILTVSEEMNTGETTYTCVAHEALPNRVTERTYDKS 576

RESULT 7  
 ID 09BUI0 PRELIMINARY; PRT; 597 AA.

AC 09BUI0;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002963; AAH02963.1; -  
 DR HSP; P01825; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein  
 SQ SEQUENCE 597 AA; 65274 MW; 2DAFABFB7055851 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 597;  
 Best Local Similarity 31.1%; Pred. No. 3.5e-34;  
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

QY 17 PTITL---PPTVTLFSSCDPR---GDAHSTIQLCLVSGSPAKVHTVTVDQGEAKN 69  
 DB 246 PLPVIAELPPKVSF---VPRDGFEGNPKRS-KLICQATGSPROIOVSWLRGKQVGS 301  
 QY 70 LPEYTT----RPKEGQTFSLQSEVNITQGMSSNTYTCVHGNSIF-EDSRKCA 123  
 DB 302 --GVTTDQVAAKESGPTTYKVTSTLTIKESDWSQSMFCRDVHRGLTFQANASMCV 359  
 QY 124 DSNPRGVSAYLSRSPFPDLFIKSPITITCLVVDLAPSKGTNLTWSRASKGVNHSRKE 183  
 DB 360 PQDDTAIRVFALPPSPASIFLTGSTLTCLVTDLT-TYDSVTISWTRONGEAVKTHNIS 418  
 QY 184 EKQRNGTLTVSTLTPVGTDMIEGETYQCRVTHPHLPALNRSTTKLPKRL-APEVYML 242  
 DB 419 ESHPNATFSAVGEASICEDDWSGERFTCTVHTDLPSPKQISRPGVALHRPDYLL 478  
 QY 243 PPSPEBTG--TTRVTCLIRGYPSSEISVQMLFNNEDHTGHTTRPQKHGTDPSPFL 300  
 DB 479 PPARQELNRESATITCLVTFSPADVFQVMQRQCPSPKXYTSAPMPPOAGRYFA 538  
 QY 301 YSRMLVNSIWEKGNLVCRVVHEALPG---SRTLEKS 335  
 DB 539 HSILTVSEEMNTGETTYTCVAHEALPNRVTERTYDKS 576

RESULT 8  
 ID 09BOB8 PRELIMINARY; PRT; 597 AA.

AC 09BOB8;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle, and Lymph;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC006180; AAH06180.1; -  
 DR EMBL; BC001872; AAH01872.1; -  
 DR HSP; P01825; 7FAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig\_5.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 25.1%; Score 465; DB 4; Length 597;  
 Best Local Similarity 31.1%; Pred. No. 3.5e-34;  
 Matches 105; Conservative 66; Mismatches 141; Indels 26; Gaps 11;

QY 17 PTITL---PPTVTLFSSCDPR---GDAHSTIQLCLVSGSPAKVHTVTVDQGEAKN 69  
 DB 246 PLPVIAELPPKVSF---VPRDGFEGNPKRS-KLICQATGSPROIOVSWLRGKQVGS 301

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QY 70 LPEYTT-----RKRRGQGFSLQSEVNTLQOMMSNTYTCYHAKNSIP-EQSSRKA 123
Db 302 --GVTTDQVGAKEKSGPTTYKVTSLTLTKESDWLSQSGMFCRDRHGLTPTQNASMCV 359
QY 124 DSNPRGVSAVLSPPSPFDLFIKSPITTLGVLDLAPSKGTVNLWISRAAGKPVNHSRKE 183
Db 360 PDODTARVFAIPSPASIFLTKSTLTCLVLDL--TDSVTLISWTRONGEAVTHTNIS 448
QY 184 EKQNRGTLVYTSPLPGTRDMLGEGTYQCRVTHPHLPRALMRSTTKLPGKTL-APETYML 242
Db 419 ESHPNATFSAVGASLTCEDDWMNGSEFCTVYTHTLDPBLKQTSIRPGVALNHPDYLL 478
QY 243 PPSPEETG--TTRYVTCLIRGFYPSHSISVQMLFNNEDHTGHTTTPRQKHGTDPSFYL 300
Db 479 PPARQQLNRESATITICLVLTGSPADVFWOMQORQPLSPKXYVTSAMPPEPQAPGRYFA 538
QY 301 YSRMLVKNKSIWEKGNLVTCRVVHAALPG---SRTEKS 335
Db 539 HSLITVSEERNMTGETTYTLCVVAHEALLPNRVTERIDVKS 576

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QY 17 PVTII---PPTVLCFHSQDPR---GDAHSTIOLCLVSGSPAKVHTW---LVGGQEAENTL 69  
 DB 246 PVPVIAELPCKVSF---VPRDGFPGNPKRS-KLICATQSPRQIVSVLSKQKQVS 301  
 QY 70 LEPTT-----RPRKGGQTFSEVNIITOGQMMSSNTYTCVHKNSIT-EDSSKCA 123  
 DB 302 -GVTTDOVQAEAKSGPTTKYKISTLTIKESDMLTOSMFCRDRHRLTPOQANSSNCV 359  
 QY 124 DSNPRGVSAYLSRSPDFLFIKSPITICLVLDLAPSKGTNLWTSASGKPVNSTRKE 183  
 DB 360 PDQDAIVFALPSPFASIFLTKSKLCIVTDLT-TDVSITISWTRNGEAVKTHNIS 418  
 QY 184 EKORNGTLVTSTLVEGRDMIEGTYQCQRYTHPHLPALMRSTTKLPGRKL-APRYML 242  
 DB 419 ESHPAVATSAVGEASICEDMNSGERFTCYTHDLPSPKQITSRPKGVALLRPDYLL 478  
 QY 243 PPSPRETG--TTRVTYCLIRGFPYSISVOMLFNNEEDHTGHHTTRPOKDHGTDPSPFL 300  
 DB 479 PPARQMLNRESATITCLVGTSPADVFQMMQKQPSPEKYVTSAPMPERQAPGRIFA 538  
 QY 301 YSRMLVNTSIMEKMLVTCRVVHEALPG--SRILEKS 335  
 DB 539 HSILTVSEEWNTGETYTCVVAHEALPRTVTERIVDKS 576

QY 18 VTIIPPTV---LFHSCDPRGDAHSTIOLCLVSGSPAKVHTW---LVGGQEAENTL 70  
 DB 135 VIVSSASTGPGSVFPLAPSSKSTSGGTALGCLVADYFEPPTVMSNALSISG---VHT 191  
 QY 71 FPYTPRPRKGGQTFSEVNIITOGQMMSSNTYTCVHKNSIT-EDSSKCA 120  
 DB 192 FPAVL-----QSSGLYSLSVTVVPSSS-LGTQTYICNVHKSNNKVKDKVPPKSCDKTH 246  
 QY 121 KC----ADSNPRGVSAYLSRSPDF-LFIKSPITICLVLDLAPSKGTNLWTSASGKPV 175  
 DB 247 TCPPCAPLGLGPPSVFLFPKPKDTLMSKPEYTCVAVDVSHEDPEKFNWYDGEV 306  
 QY 176 VNHSTRKEKORNGTLVTSTLVEGRDMIEGTYQCQRYTHPHLPALMRSTTKLPGRKL 235  
 DB 307 HNAKTPREQYNSFVAVSVTLVHQPWLNGEKYKCKVSNALAPAEIKTISKAKGQR 366  
 QY 236 APBYVMLPSPDEE-TCTTIVTCLIRGFPYSISVOMLFNNEEDHTGHHTTRPOKDHGT 294  
 DB 367 EPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEMSNQGPEN--NYKTPVYLD--S 422  
 QY 295 DPSFPLYSRMLVNTSIMEKMLVTCRVVHEALPGSRILEKSHIYAG 341  
 DB 423 DGSFPLYSRMLVNTSIMEKMLVTCRVVHEALPGSRILEKSHIYAG 468

## RESULT 14

Q727P5 PRELIMINARY; PRT; 469 AA.

ID Q727P5  
 AC Q727P5  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC051328; AA051328.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 469 AA; 51395 MW; C6D5B812BAAR795C CRC64;

Query Match 24.5%; Score 455; DB 4; Length 469;  
 Best Local Similarity 33.4%; Pred. No. 2.1e-33;  
 Matches 116; Conservative 63; Mismatches 132; Indels 36; Gaps 12;

## RESULT 15

Q725W1 PRELIMINARY; PRT; 470 AA.

ID Q725W1  
 AC Q725W1  
 DT 01-OCT-2003 (Tremblrel. 25, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX Strausberg R.;  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC053984; AA053984.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 24.5%; Score 455; DB 4; Length 470;  
 Best Local Similarity 33.4%; Pred. No. 2.1e-33;

Matches 116; Conservative 63; Mismatches 132; Indels 36; Gaps 12;

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OY      18  VTIIPTVK--LPHSSGDPKGDASHSTIQLCLVSGFSPAKVHYTW----LYDQGEAENL 70
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      136 VTVSSASTKGPSVFPPLAPSKSTGGTALGCLVKDIFPEPVTVSMNSGALTSG--VHT 192
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      71  FPYTRPRREGGQTFSLOSEVNIIOGOWMSNTYTCHVKNNGSIFE-----DSSR 120
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      193 FPAVL---QSSGLYSLSSVTVTPSSS-LGTQTYICNVNKKPSNTKYDKKVEPKSCDKTH 247
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      121 KC---ADSNRQVSATYSRSPPD-LFIRKSPITTCVVDLAPSKGTNYLTWSRAGKP 175
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      248 TCPCPAPABELIGPSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMVYVDGVEV 307
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      176 VNSIRKEKQKQNGTLVTSTLPVGTQDWIEGETYQCRVTHPHLPALMRSTTKLPQKRL 235
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      308 HNAKTKPREEQYNSTYRVSVTLVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 367
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      236 APEVYMLPRSPPE-TGTRITVTCIRGFYPSISVQWLFNNEEDHTGHTTTTRPQKDHGT 294
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      368 EPQVYTLPPSRDELTKQVSLTCLVKGYPBDIAVEWESNGQPEN--NYKTTPEVLD--S 423
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
OY      295 DPSEFLYSRMLVNSIWEKGNLVTCRVVHEALPGSRITLKSILHYSAG 341
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      424 DGSFFLYSKLTVDKSRWQGNVFCSVNHEALNHHT-QKSLSLSPG 469
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
```

Search completed: February 26, 2004, 12:00:53  
Job time : 48 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:43:41 ; Search time 18 seconds  
(without alignments)  
989.333 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856  
Sequence: 1 EFFFFHHHTLSPESGPVTL.....HEALPGSRTEKLHYSAGN 342

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1038.5	56.0	428 1 EPC_HUMAN	P01854 homo sapien
2	787.5	41.4	429 1 EPC_RAT	P01855 rattus norv
3	751	40.5	421 1 EPC_MOUSE	P06336 mus musculu
4	497.5	26.8	479 1 MUCM_MOUSE	P04221 oryctolagus
5	495.5	26.7	458 1 MUCM_RABIT	P03988 oryctolagus
6	486.5	26.2	326 1 GC2_HUMAN	P01859 homo sapien
7	483	26.0	454 1 MUC_MESAT	P06337 mesocricetu
8	476	25.6	327 1 GC4_HUMAN	P01861 homo sapien
9	475.5	25.6	454 1 MUC_HUMAN	P01871 homo sapien
10	469	25.3	455 1 MUCM_MOUSE	P01872 mus musculu
11	469	25.3	476 1 MUCM_MOUSE	P01873 mus musculu
12	460	24.8	391 1 MUCB_HUMAN	P04220 homo sapien
13	454	24.5	330 1 GCL_HUMAN	P01857 homo sapien
14	450	24.2	457 1 MUC_MOUSE	P07056 eunus mur
15	444	23.9	450 1 MUC_CANFA	P01874 canis fami
16	443.5	23.9	322 1 GEA_RAT	P20760 rattus norv
17	437.5	23.6	323 1 GC_RABIT	P01870 oryctolagus
18	436.5	23.5	326 1 GCL_RAT	P07055 rattus norv
19	428	23.1	329 1 GCL_MOUSE	P07056 rattus norv
20	424.5	22.9	329 1 GCL_MOUSE	P01862 cavia porce
21	421	22.7	335 1 GCAB_MOUSE	P01864 mus musculu
22	415.5	22.4	324 1 GCL_MOUSE	P01868 mus musculu
23	415.5	22.4	393 1 GCL_MOUSE	P01868 mus musculu
24	401.5	21.6	290 1 GCL_HUMAN	P01860 homo sapien
25	399.5	21.5	336 1 GCB_MOUSE	P01866 mus musculu
26	399.5	21.5	405 1 GCB_MOUSE	P01867 mus musculu
27	397	21.4	329 1 GCB_MOUSE	P22463 mus musculu
28	395.5	21.3	330 1 GCA_MOUSE	P01863 mus musculu
29	395.5	21.3	339 1 GCA_MOUSE	P01865 mus musculu
30	392	21.1	338 1 GCB_MOUSE	P03987 mus musculu
31	384	20.7	333 1 GCB_MOUSE	P07057 rattus norv
32	371.5	20.0	438 1 HVC2_HETER	P23085 heterodontu
33	369.5	19.9	340 1 ALC2_HUMAN	P01877 homo sapien

34	358	19.3	353 1 ALC1_HUMAN	P01876 homo sapien
35	352.5	19.0	438 1 HVC3_HETER	P23087 heterodontu
36	352.5	19.0	461 1 HVC3_HETER	P23088 heterodontu
37	348	18.8	353 1 ALC1_GORGO	P20758 gorilla gor
38	346.5	18.7	370 1 HVC1_HETER	P23084 heterodontu
39	343.5	18.5	393 1 HVC3_HETER	P23086 heterodontu
40	341	18.4	446 1 MDC_CHICK	P01875 gallus gall
41	335.5	18.1	344 1 ALC_MOUSE	P01878 mus musculu
42	277	14.9	481 1 MUCM_MOUSE	P23735 ictalurus p
43	260	14.0	299 1 ALC_RABIT	P01879 oryctolagus
44	227.5	12.3	383 1 DTC_HUMAN	P01880 homo sapien
45	167.5	9.0	503 1 SHS1_HUMAN	P78324 h protein-c

## ALIGNMENTS

RESULT 1	ID	EPIC_HUMAN	STANDARD	PRT	428 AA
AC	P01854	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	21-OCT-2003 (Rel. 42, Last annotation update)				
DE	15 epsilon chain C region.				
GN	IGH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8336887; PubMed=6300763;				
RA	Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,				
RA	Kikuchi M., Sugino Y., Nishida Y., Honjo T.;				
RT	"Molecular cloning and nucleotide sequencing of human immunoglobulin				
RT	epsilon chain cDNA."				
RL	Nucleic Acids Res. 11:719-726(1983).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND VARIANT LEU-359.				
RX	MEDLINE=83001945; PubMed=6288268;				
RA	Max E.E., Batley U., Ney R., Kirsch I.R., Leder P.;				
RT	"Duplication and deletion in the human immunoglobulin epsilon genes."				
RL	Cell 29:691-699(1982).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84236029; PubMed=6234164;				
RA	Flanagan J.G., Rabbits T.H.;				
RT	"The sequence of a human immunoglobulin epsilon heavy chain constant				
RT	region gene, and evidence for three non-allelic genes."				
RL	EMBO J. 1:655-660(1982).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=84207910; PubMed=6327276;				
RA	Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;				
RT	"Long terminal repeat-like elements flank a human immunoglobulin				
RT	epsilon pseudogene that lacks introns."				
RL	EMBO J. 1:1539-1544(1982).				
RN	[5]				
RP	PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).				
RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;				
RL	(In) Bach M.K. (eds.);				
RT	Immediate hypersensitivity: modern concepts and developments, pp.1-36,				
RL	Marcel Dekker, New York (1978).				
RN	[6]				
RP	SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.				
RX	MEDLINE=83065234; PubMed=6815656;				
RA	Kerten U.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.;				
RA	Bell L.O., Gould H.U.;				
RT	"Cloning and sequence determination of the gene for the human				
RT	immunoglobulin epsilon chain expressed in a myeloma cell line."				
RL	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RN	[7]				

3D-STRUCTURE MODELING.  
 MEDLINE=87089848; PubMed=3796618;  
 Padian E.A., Davies D.R.;  
 "A model of the Fc of immunoglobulin E";  
 Mol. Immunol. 23:1063-1075(1986)  
 -1- SIMILARITY: Contains 4 immunoglobulin-like domains.  
 -----  
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 CC  
 DR EMBL; I00022; AAB59424.1; ALT\_INIT.  
 DR PIR; A22771; EMTU.  
 DR PDB; 1IG8; 15-JUL-92.  
 DR PDB; 1FP5; 30-JAN-02.  
 DR PDB; 1G84; 16-MAY-01.  
 DR PDB; 1OOV; 18-SEP-02.  
 DR Genew; HGNC:5522; IGHE.  
 DR MIM; 147180; -.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00407; IgC1; 4.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW 3D-structure; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 103  
 FT DOMAIN 112 210  
 FT DOMAIN 214 318  
 FT DOMAIN 324 423  
 FT DISULFID 15 105  
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 FT CARBOHYD 49 49  
 FT CARBOHYD 99 99  
 FT CARBOHYD 146 146  
 FT CARBOHYD 252 252  
 FT CARBOHYD 275 275  
 FT CARBOHYD 359 359  
 FT STRAND 110 110  
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 FT HELIX 122 124  
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 FT TURN 168 169  
 FT STRAND 172 181  
 FT HELIX 182 186  
 FT TURN 187 188  
 FT STRAND 192 196  
 FT TURN 198 199  
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 FT STRAND 205 207  
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FT TURN 226 229  
 FT TURN 231 232  
 FT STRAND 236 242  
 FT STRAND 252 252  
 FT STRAND 255 257  
 FT TURN 258 259  
 FT STRAND 260 260  
 FT TURN 265 266  
 FT STRAND 271 274  
 FT TURN 275 276  
 FT STRAND 277 285  
 FT HELIX 288 293  
 FT TURN 294 294  
 FT STRAND 297 302  
 FT TURN 304 305  
 FT STRAND 310 314  
 FT STRAND 322 322  
 FT STRAND 325 329  
 FT STRAND 334 337  
 FT HELIX 334 348  
 FT STRAND 340 346  
 FT STRAND 350 351  
 FT STRAND 356 360  
 FT TURN 366 369  
 FT STRAND 374 374  
 FT STRAND 377 378  
 FT TURN 380 381  
 FT STRAND 384 385  
 FT STRAND 387 393  
 FT STRAND 394 398  
 FT HELIX 394 400  
 FT TURN 399 400  
 FT STRAND 404 408  
 FT STRAND 418 421  
 SQ SEQUENCE 428 AA; 47019 MW; 25C4CA072A558A0 CRC64;  
 Query Match 56.0%; Score 1038.5; DB 1; Length 428;  
 Best Local Similarity 62.4%; Pred. No. 1.8e-72;  
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;  
 QY 22 PPTVKLFHSSCDPRGDAHSTIQLCLVSGFSPAKYVWLVQGEAENLFPYTPRKKEG 81  
 DB 111 PPTVKLQSSCDGGHFPPTIQLCLVSGYTPGTINITWLEDDQVMD--VLDSTASTQ 168  
 QY 82 GQTFSLQSEVNTTQGMNSNTTYTCHVKNKSIFFDSRKKCDNSPRGVSAIATSPSPD 141  
 DB 169 GELASQSELTLSQKMLSDRTTYQVYTGHTFEDSTKCDNSPRGVSAIATSPSPD 228  
 QY 142 LFTKSPFTTCVVDLAPSKGTVNLWSPASGPNVHSTRKEKORNGTLVTSILPYGT 201  
 DB 229 LFTKSPFTTCVVDLAPSKGTVNLWSPASGPNVHSTRKEKORNGTLVTSILPYGT 288  
 QY 202 RDMIBETTYQCRVTHPLPRALMRSTTKLPGKELAPBYVMDPPSPBETGT--TRIVTCL 259  
 DB 289 RDMIBETTYQCRVTHPLPRALMRSTTKSGRAAPBYVAF--ATPEWPSRDKRTLACL 347  
 QY 260 RGFYSEISVQWLFNNEEDHTGHTTTPQKHGTDPSFTLSPMLVKNKSIWEKGLVTC 319  
 DB 348 QNFMPEDISVQWLFNNEEDHTGHTTTPQKHGTDPSFTLSPMLVKNKSIWEKGLVTC 405  
 QY 320 RVVHEALPGSRILEKSLATYSAG 341  
 DB 406 RAVHEAASPGQTVQRAVSVPNG 427  
 RESULT 2  
 EPC\_RAT STANDARD, PRT, 429 AA.  
 ID EPC\_RAT  
 AC P01855;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig epsilon chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 [1]  
 RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).  
 RC STRAIN=LOU/C/MSL;  
 RX MEDLINE=83064537; PubMed=6292865;  
 RA Hellman L., Petersen U., Engstroem A., Karlsson T., Bennich H.;  
 RT "Structure and evolution of the heavy chain from rat immunoglobulin  
 E.";  
 RL Nucleic Acids Res. 10:6041-6049(1982).  
 RN [2]  
 RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).  
 RX MEDLINE=83182019; PubMed=6820340;  
 RA Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;  
 RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:  
 RT construction, identification, and DNA sequence.";  
 RL DNA 1:335-343(1982).  
 RN [3]  
 RP SEQUENCE OF 205-306 FROM N.A.  
 RX MEDLINE=82174576; PubMed=6803238;  
 RA Hellman L., Petersen U., Bennich H.;  
 RT "Characterization and molecular cloning of the mRNA for the heavy  
 RT (epsilon) chain of rat immunoglobulin E.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).  
 CC -1- SIMILARITY: Contains 4 immunoglobulin-like domains.  
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 CC -----  
 CC EMBL: J00744; AAA41379.1; ALT\_INIT.  
 DR PIR: A93442; EHRT.  
 DR HSSP: P01854; 1IGR.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR Pfam: PF00047; IG1.4.  
 DR SMART: SM00407; Igcl. 1.  
 DR PROSITE: PSS0835; IG-1like; 4.  
 DR PROSITE: PS00290; IG\_MHC; 3.  
 KW Immunoglobulin domain; Immunoglobulin C region; Repeat.  
 FT NON\_TER 1 1  
 FT DOMAIN 6 89 IG-LIKE 1.  
 FT DOMAIN 103 201 IG-LIKE 2.  
 FT DOMAIN 205 305 IG-LIKE 3.  
 FT DOMAIN 314 414 IG-LIKE 4.  
 FT CONFLICT 168 168 R -> N (IN REF. 2).  
 FT CONFLICT 308 308 P -> L (IN REF. 2).  
 SQ SEQUENCE 429 AA; 48671 MW; D2970B34E8FA72B0 CRC64;

Query Match 41.4%; Score 767.5; DB 1; Length 429;  
 Best Local Similarity 45.8%; Pred. No. 1,1e-51;  
 Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;  
 OY 17 PVTIIPFYKLFHSSCDPRGDAHSTIQLCLVSGSPAKVHTWMLVDGCEANLFPYTR 76  
 DB 97 PNIRKPTVDLHSSCDPWA-PHSTIQLYCFYGHIGQDVSHMLMDRKI-----YTH 150  
 OY 77 PK-----REGGQTFSLQSEVNITQOGWMSNTYTGAVKNGSIFEDSKKADSNPRGVA 132  
 DB 151 AONVLIKEGKGLASTYSRLNITQOOWMSSTFTCKVTSQGENYMAHTRCSDDEPRGVIT 210  
 OY 133 YLSRSPFDLFRKSPFTICLVVDLAPSKGVNLTWMSBASGKPVNHSRKEKXONGTLT 192  
 DB 211 YIIPSPDLVYENGPKLCTVLDL-ESEENITVWVAZERKKSISASQBSTKHNAITS 269  
 OY 193 VTSITLPGTRDWIESEETQOCRTVHPHLPALMRSTTKLPGKRLAEVYMLPPSPETGTT 252  
 DB 270 ITSILPVAKDWIEBEGVQCRVDHDPFKPIVRSITKAPGRSAPEVVFLLPPEEEKDK 329

RESULT 3  
 EPC\_MOUSE STANDARD; PRT; 421 AA.  
 ID EPC\_MOUSE  
 AC P06336; P01856;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-1999 (Rel. 38, Last annotation update)  
 DE Ig epsilon chain C region.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84236092; PubMed=6329728;  
 RA Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;  
 RT "The nucleotide sequence of the mouse immunoglobulin epsilon gene:  
 RT comparison with the human epsilon gene sequence.";  
 RL EMOB J. 1:1117-1123(1982).  
 RN [2]  
 RP REVISIONS.  
 RA Honjo T.;  
 RL Submitted (APR-1986) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 34-421 FROM N.A.  
 RX MEDLINE=83117774; PubMed=6818553;  
 RA Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;  
 RT "Cloning and nucleotide sequence of mouse immunoglobulin epsilon  
 RT chain cDNA.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).  
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 CC -----  
 CC EMBL: X01857; CA25977.1; -  
 DR PIR: A02144; EHMS.  
 DR PIR: A02145; EHMS.  
 DR HSSP: P01854; 1IGR.  
 DR InterPro: IPR007110; IG-1like.  
 DR InterPro: IPR003597; IG\_C1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR Pfam: PF00047; IG1.4.  
 DR SMART: SM00407; Igcl. 2.  
 DR PROSITE: PSS0835; IG-1like; 4.  
 DR PROSITE: PS00290; IG\_MHC; 3.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 90 CH1.  
 FT DOMAIN 91 197 CH2.  
 FT DOMAIN 198 304 CH3.  
 FT DOMAIN 305 421 CH4.  
 FT DISULFID 23 75 BY SIMILARITY.  
 FT DISULFID 121 180 BY SIMILARITY.  
 FT DISULFID 226 285 BY SIMILARITY.  
 FT DISULFID 330 392 BY SIMILARITY.  
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 421 AA; 47320 MW; 8F909E1F30A05B47 CRC64;

Query Match 40.5%; Score 751; DB 1; Length 421;  
 Best Local Similarity 44.8%; Pred. No. 2e-50;  
 Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

QY 2 FHHHHHTLSLSPES-----GPTTTPYKLFHSSGCDPRGASHITDLCVSGSPSPAKV 56  
 DB 73 FICHVTHPPSPFNSSRTILVRPVNITEPTIELHSSCDPNA-FHSTIQYCFYGHILNDV 131  
 QY 57 HTWLVDDGAEHLFFYTRPRKGGQTSLOSEVNTTGGMSSNTYTCVKNHNGSIFE 116  
 DB 132 SYSLMDREKIDTDLTAQVLKEE-GKLASTCKMLTTRBQWMSSTFTCKVTSGVDYL 190  
 QY 117 DSRKCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWSPRAGPV 176  
 DB 191 ATRRCPDHEPRGVITVLLPSPDLQNGAPKRLCTLVVDLSEK-NVNVWNGEKKTSV 249  
 QY 177 NNSTRKEKQKNGTLVTSTLPVGRDWEGETYQCRVTHPLPALMRSTTKLPKRLA 236  
 DB 250 SASQWYTKHNNATSTISILPVADWIEGYQCTVDHPFPKPVAYSIKTKGQSA 309  
 QY 237 PEVYMLPSPPEETGTTRVTCILRGFYSSEISVQWLFNNEEDHGHHTTRPOKHGDP 296  
 DB 310 PEVYVPPPEESEDKRTITCLIQNFPEPDISVQWLGQCKLINSQHSHTTTPDKNSNG 369  
 QY 297 SPFLYSRLMVKNSIWEKGNLVCRRVHEALPDSRTLEKSLHYSAGN 342  
 DB 370 GFIFSRLEVAKTLWQRKQFQVTHALQKPRKLEKTIKSTLGN 415

RESULT 4  
 MUCM RABIT STANDARD; PRT; 479 AA.

AC P04221;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 19 mu chain C region membrane-bound form.  
 OS Oryctolagus cuniculus (Rabbit)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 ON NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A. (A2 ALLOTYPED).  
 RX MEDLINE=84088930; PubMed=6418803;  
 RA Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.  
 RT "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain  
 of Vha2 allotype: comparisons with Vha1 and membrane mu sequences."  
 RL J. Immunol. 132:490-495 (1984).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=During differentiation, B lymphocytes switch from  
 CC expression of isoform Membrane-bound to isoform Secreted;  
 CC Name=Membrane-bound;  
 CC IsoId=P04221-1; Sequence=Displayed;  
 CC Name=Secreted;  
 CC IsoId=P03988-1; Sequence=External;  
 CC -----  
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CC -----  
 DR EMBL: K01357; AAA31293.1; --  
 DR PIR: A02165; MRRBM.  
 DR HSSP: P01842; 7PAB.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003597; Ig\_c1.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00407; IgC1; 2.  
 DR PROSITE: PSS0835; IG\_LIKE; 4.  
 DR PROSITE: PSS0229; IG\_MHC; 3.  
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KM Alternative splicing; Transmembrane.

FT NON TER 1  
 FT DOMAIN 1 106 CH1.  
 FT DOMAIN 107 222 CH2.  
 FT DOMAIN 223 327 CH3.  
 FT DOMAIN 328 458 CH4.  
 FT TRANSMEM 459 476 POTENTIAL.  
 FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).  
 FT DISULFID 28 90 BY SIMILARITY.  
 FT DISULFID 137 200 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT DISULFID 219 219 BY SIMILARITY.  
 FT DISULFID 249 308 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT DISULFID 296 296 BY SIMILARITY.  
 FT DISULFID 356 418 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 479 AA; 52351 MW; 689C637A47BE18FC CRC64;

Query Match 26.8%; Score 497.5; DB 1; Length 479;  
 Best Local Similarity 32.9%; Pred. No. 6.5e-31;  
 Matches 117; Conservative 61; Mismatches 153; Indels 25; Gaps 10;

QY 5 HHHHTLSLSPSGPV-PIIPPTVLFHSSGCDPR---GDASHITDLCVSGSPSPAKVHT 59  
 DB 94 HSNRNDRLVSPVDELFPNVSVF--IPRDSFGSGSTRSRLLCOATGSPKQISVS 150  
 QY 60 WLVDDGAEHLN-LFYTTRPRKGGQTSLOSEVNTTGGMSSNTYTCVKNHNGSIFE 116  
 DB 151 WLVDDGQVREGVLTKEVBAETKQAGPATFSISMLTTSQSLYTCRVDDHGIFPD 210  
 QY 117 DS---SRKCADSNPRGVSAYLSRSPFDLFIKSPITITCLVVDLAPSKGTVNLWSPRAG 173  
 DB 211 KNVSMSESGSTTSPSPDQVPLPASPADPFLKSNARLICLVTDLT-TYGSINIWSASHNG 269  
 QY 174 KPVNHSSTRKEKQKNGTLVTSTLPVGRDWEGETYQCRVTHPLPALMRSTTKLPK 233  
 DB 270 KALDTMNTSHSPNATFSMGEASVCADWMSGQFTVTHADLPFLKTKISK--SR 327  
 QY 234 RLA---PEVYMLPSPPEE--TGTRVTCILRGFYSSEISVQWLFNNEEDHGHHTTRP 288  
 DB 328 EVAKHPPAYVVLPPABQLVLRSAATVTCLVGFSADVFVQOGRGQLSDKVTYSAP 387  
 QY 289 QKDHGTPSPFLYSRLMVKNSIWEKGNLVCRRVHEALP---GSRTLEKSLHYSAG 341  
 DB 388 APEPQAPGLYFTHSTILTVBEDMNSGETFTCVVGHGHALPHMTERIVDSTGEVNG 443

RESULT 5  
 MUCM RABIT STANDARD; PRT; 458 AA.

AC P03988;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 19 mu chain C region secreted form.  
 OS Oryctolagus cuniculus (Rabbit)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



RL Mol. Immunol. 16:923-925 (1979).  
 RN [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Part D.M.;  
 RL Submitted (MAR-1980) to the PIR data bank.  
 RN [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RX MEDLINE=95255298; PubMed=77371190;  
 RA Stoppani M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RT "Disulphide bridges of the heavy chain of human anti-flavin monoclonal  
 immunoglobulin";  
 RL Eur. J. Biochem. 228:886-893 (1995).  
 RN [9]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225 (1971).  
 RN [10]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=69064124; PubMed=5782707;  
 RA Frangione B., Milstein C., Pink J.R.L.;  
 RT "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148 (1969).  
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 CC -----  
 DR EMBL; J00230; AAB59393.1; -  
 DR PIR; A93906; G2HU.  
 DR HSSP; P01857; 1PCL.  
 DR Genew; HGNC:5526; IGHG2.  
 DR MIM; 147110; -  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006555; F:immune response; NAS.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGH1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KM Immunoglobulin domain; Immunoglobulin C region.  
 FT NON TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT DISULFID 156 156  
 FT SITE 326 326  
 FT MOD RES 326 326  
 FT VARIANT 60 60  
 FT NON TER 1 1  
 FT DOMAIN 1 105 CH1.  
 FT DOMAIN 106 218 CH2.  
 FT DOMAIN 219 324 CH3.  
 FT DOMAIN 325 454 CH4.  
 FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).  
 FT DISULFID 27 88 BY SIMILARITY.  
 FT DISULFID 135 198 BY SIMILARITY.  
 FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT CONFLICT 109 109 C -> S (IN REF. 3).  
 FT SEQUENCE 326 AA; 35884 MW; 8310876C6878CF9C CRC64;  
 Query Match 26.2%; Score 486.5; DB 1; Length 326;  
 Best Local Similarity 36.2%; Pred. No. 2,8e-30;  
 Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGAHSTIOLLCYVSGSPAKVHTW----LVQGAENLFPYTRPKREGGOTFSLOSE 90  
 DB 16 RSTESSTALGCLVKKVDFPEPVVSNNSGALISG---VHTFAVL---QSSGLSTLSV 68  
 QY 91 VNTTGGQMSNSTTTCVTKH---NSIFEDSSRKCADSNP-----RGVAYLSRPSPF 140  
 DB 69 VTPSSNF-GRQYTCVNDHREPNTYKDKVERKCCVCEPCPPAPVAGPSVLEFPPEK 127  
 QY 141 D-LFIRSPITTCIVLDIAPSKGTVALTWSRASGKPVNSTREKQKRGITVLTSTPV 199  
 DB 128 DTLWISSTPEVTCVVDVSHEDPEVQFNWYGVGVHNAKTKPREQFNSTFRVSVLTV 187  
 QY 200 GTRWIEGTYQCRVTHPHLPALMASTYLPCKRLAPVYVLPSPPE-TEITTVYCL 258  
 DB 188 VQDMLNGKRYCKVSKGLPAPLEKISTKQPREPVYLLPSREMTXNVSLTCL 247  
 QY 259 IRGFYPSPISYQMLFNNEEDHTGHTTTPPOKDHGTPSPFPLYSRLYKKSIMKGNLVT 318  
 DB 248 VKGFYPSDIAVEMESNGOPEN--NYKTPPMD--SDGSFFLYSKLTVDKSRWQGANVFS 303  
 QY 319 CRVVEALPQSRTEKSLHYSAG 341  
 DB 304 CSVNEBALNHYT-QKSLSLSPG 325  
 RESULT 7  
 MUC\_MESAU STANDARD; PRT; 454 AA.  
 ID MUC\_MESAU  
 AC P06337;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig mu chain C region.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85297761; PubMed=2994005;  
 RA McGilre K.L., Duncan W.R., Tucker P.W.;  
 RT "Phylogenetic conservation of immunoglobulin heavy chains: direct  
 RT comparison of hamster and mouse Cmu genes.";  
 RL Nucleic Acids Res. 13:5611-5628 (1985).  
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 CC -----  
 DR EMBL; X02804; CAA26574.1; -  
 DR HSSP; P01854; IIGB.  
 DR InterPro; IPR007110; Ig-1like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00407; IGH1; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; 3.  
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON TER 1 1  
 FT DOMAIN 1 105 CH1.  
 FT DOMAIN 106 218 CH2.  
 FT DOMAIN 219 324 CH3.  
 FT DOMAIN 325 454 CH4.  
 FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).  
 FT DISULFID 27 88 BY SIMILARITY.  
 FT DISULFID 135 198 BY SIMILARITY.  
 FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).

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FT DISULFID 245 304 BY SIMILARITY.
FT DISULFID 292 414 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 332 414 BY SIMILARITY.
FT DISULFID 453 453 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 454 AA; 50196 MW; 4DA2134612BE1469 CRC64;

Query Match 26.0%; Score 483; DB 1; Length 454;
Best Local Similarity 34.0%; Pred. No. 7,9e-30;
Matches 119; Conservative 58; Mismatches 147; Indels 26; Gaps 10;

QY 5 HHNHT---LSLPSGPTVITPTPTKLFHSSCDP-RGDASTITQLCLVSGFSPAKVHTW 60
DB 91 HNGNTNKDLRVP-IPVTEANPNVSVFVPSRDASGPAFRKSRFLFCEASNFSPKQITVSW 149
QY 61 LVDGQEAENLFP---PYTRPKRGQPTSLQSEVNITQGMWSNNTYCHYKNGSIF-E 116
DB 150 LRDKPVKSGFTTEVTPEDESGPRITKIVSTLITPSDMANSVTTCRYDRGLTFWK 209
QY 117 DSRKCADSNPRGSAVLSRSPDPLTRKSPITTCVLVDLAPSKGTVNTWSPASGPV 176
DB 210 NVSSICAPSPSTDIQAFPIPPSPFVIGFINKSATLCLVATNLA-TYDITLINSWSSRSSEPL 268
QY 177 NHTSRKEKORNGTLTVSTLPVGRMDIEGETVOCRTHTHLR-----ALMRSTTKL 230
DB 269 ETKIKLTSHPNGFSAIGEANVCEDWDSKEFVCTVTHDLSPPQKPKISKRENNKT 328
QY 231 PFKSLAPEVYMLPSPPEE-TGTRITVCLIRGFYPSHSISYQMLFNNEDHTGHTTTRP 288
DB 329 P-----PAVYQOPLAREQLIRRESATVCLVKGFSPADIFQYMLQRGQPLSQDKYVTSAP 363
QY 289 QKDHGTDSFPLYSRLMVKNSIKWEKGNLYTRVYHEALP---GSRITLKS 335
DB 384 MREPOAPHLVFTHSVLTVEEENSGEYTYTCVVGHEALPHVNTERTVDRS 433

RESULT 8
GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861.1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE IG gamma-4 chain C region.
GN IGH4.
OS Homo sapiens (Human).
OC Buteyria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCI_TaxID=9606;
OX NCI_TaxID=9606;
RN 1
RP MEDLINE=63157104; PubMed=6299662;
RA Eliason J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN 2
RP SEQUENCE OF 1-30 AND 81-326.
RA MEDLINE=70207560; PubMed=4192699;
RT Pink J.R.L., Buttery S.H., de Vries G.M., Milestein C.;
RT "Human immunoglobulin subclases. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC or send an email to license@isb-sib.ch.)
CC -----
CC EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PIR; IADO; 16-SEP-98.
DR Genbank; HGNC:5528; IGH4.
DR MIM; 147130.
DR GO; GO:0005824; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig1.3.
DR SMART; SM00407; Igcl.2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KM Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD11BF208E7A CRC64;

Query Match 25.6%; Score 476; DB 1; Length 327;
Best Local Similarity 35.8%; Pred. No. 1,8e-29;
Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGDASTITQLCLVSGFSPAKVHTW---LVDGQEAENLFPYTRPKRGQPTSLQSE 90
DB 16 RSTSTSTALGLVVDYFPEPTVYVSNMGALTSG---VHTPPAVL---QSSGLYSLSV 68
QY 91 VNITQGMWSNNTYCHYKNGSIFEDSSRRCADSNP-----RGSAYLSRSP 139
DB 69 VIVPSSS-LGRTTYICNDVDPKSPNTKVDKVESKGPCCPCAPBFLGFSVFLFPKP 127
QY 140 PD-LFIRKSPITTCVLVDLAPSKGTVNTWSPASGPVNHSTRKEKQNGTLTVTSTLP 198
DB 128 KDTLMISTPPEVTCVVDVDSQSDPEVQFNWYVDGVEVHNAKTKPREQFNSTYRVSVLT 187
QY 199 VGTTRWIGETVQCVTHPHLPALMRSTTLPGKRLAPRYVMPPSPPE-TGTRITVTC 257
DB 188 VHQDWLNGEKYKCVNKGKPSISLEKTSIPAKQPREPQYTLPPSOEEMTKQVSLTC 247
QY 256 LIRGFYPSHSISYQMLFNNEDHTGHTTTRPQKDHGTDPSPFLYSRLMVKNSIKWEKGNLY 317
DB 248 LVKGFYPSDIAVEMSNQCPEN-NYKTTPEVLD--SDGSFPLSRLTVDSRWQEGVVF 303
QY 318 TTRVYHEALPGSRITLKSILHSAG 341
DB 304 SCVYHEALHHNHT-QKSLSLSLG 326

RESULT 9
MOC_HUMAN STANDARD; PRT; 454 AA.
AC P01871.1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 01-FEB-1991 (Rel. 17, last sequence update)
DT 15-MAR-2004 (Rel. 43, last annotation update)
DE IG mu chain C region.
GN IGHM.
OS Homo sapiens (Human).

```



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-434 FROM N.A.  
 RX MEDLINE=9032450; PubMed=2115996;  
 RA Friedlander R.M., Nussenzweig M.C., Leder P.;  
 RT "Complete nucleotide sequence of the membrane form of the human IGM  
 heavy chain.";  
 RL Nucleic Acids Res. 18:4278-4278(1990).  
 RN [2]  
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN GAL).  
 RX MEDLINE=5059123; PubMed=4803843;  
 RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;  
 RT "The primary structure of a monoclonal IGM-immunoglobulin  
 (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-  
 type), subgroup H III. Architecture of the complete IGM-molecule.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).  
 RN [3]  
 RP REVISIONS (GAL).  
 RX MEDLINE=8106716; PubMed=6777162;  
 RA Mhaesco E., Barnikol-Watanabe S., Barnikol H.U., Mhaesco C.,  
 RA Hilschmann N.;  
 RT "The primary structure of the constant part of mu-chain-disease  
 protein BOT.";  
 RL Eur. J. Biochem. 111:275-286(1980).  
 RN [4]  
 RP SEQUENCE (WALDENSTROM'S CU), DISULFIDE BONDS, AND CARBOHYDRATES.  
 RX MEDLINE=7400511; PubMed=4742735;  
 RA Putnam F.W., Florent G., Paul C., Shinoda T., Shimizu A.;  
 RT "Complete amino acid sequence of the mu heavy chain of a human IGM  
 immunoglobulin.";  
 RL Science 182:287-291(1973).  
 RN [5]  
 RP PARTIAL SEQUENCE FROM N.A.  
 RX MEDLINE=82059479; PubMed=6795593;  
 RA Rabbits T.H., Forster A., Milstein C.P.;  
 RT "Human immunoglobulin heavy chain genes: evolutionary comparisons of  
 C mu, C delta and C gamma genes and associated switch sequences.";  
 RL Nucleic Acids Res. 9:4509-4524(1981).  
 RN [6]  
 RP SEQUENCE OF 299-387 AND 438-454 FROM N.A.  
 RX MEDLINE=81077306; PubMed=6777778;  
 RA Dolby T.W., Devuono J., Croce C.M.;  
 RT "Cloning and partial nucleotide sequence of human immunoglobulin mu  
 chain cDNA from B cells and mouse-human hybridomas.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980).  
 CC -1- MISCELLANEOUS: All 4 combinations of the S/G and V/G polymorphisms  
 at positions 192 and 216 have been observed in human mu chains.  
 CC -----  
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 CC -----  
 DR EMBL; X17115; CAA34971.1; ALT\_SEQ.  
 DR EMBL; X57086; -; NOT\_ANNOTATED\_CDS.  
 DR HSSP; P01857; 1FCL.  
 DR Gene; HGNC:5541; IGHN.  
 DR MIM; 147020.  
 DR GlycosuiteDB; P01871; -.  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; P:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; Ig\_4.  
 DR SMART; SM00407; Igcl; 3.  
 DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; 3.  
 KM Immunoglobulin domain, Immunoglobulin C region; Glycoprotein;  
 KW Polymorphism.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 105 CH1.  
 FT DOMAIN 106 218 CH2.  
 FT DOMAIN 219 324 CH3.  
 FT DOMAIN 325 454 CH4.  
 FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN).  
 FT DISULFID 28 88 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 135 198 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 215 215 INTERCHAIN (WITH HEAVY CHAIN IN ANOTHER  
 FT DISULFID 245 304 SUBUNIT).  
 FT DISULFID 292 292 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 352 414 INTERCHAIN (WITH HEAVY CHAIN).  
 FT DISULFID 453 453 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .).  
 FT VARIANT 192 192 S -> G.  
 FT VARIANT 192 192 /FTID=VAR\_003903.  
 FT VARIANT 216 216 V -> G (in dbSNP:12365).  
 FT VARIANT 216 216 /FTID=VAR\_003904.  
 SQ SEQUENCE 454 AA, 49556 MW, 2167228056922E CRC64,  
 FT VARIANT 216 216 /FTID=VAR\_003904.  
 Query Match 25.6%; Score 475.5; DB 1; Length 454;  
 Best local similarity 31.4%; Pred. No. 3e-29;  
 Matches 106; Conservative 65; Mismatches 142; Indels 25; Gaps 10;  
 QY 17 PVTIT---PPTVGLFHSSCDPR---GDAHSTIGLICLVSGSPAKVHTWLVDCQEAEN 69  
 DB 102 PLRVIALPDKVSVF---VPRPDGFGNRSRSLKICQATGSPQIQVSWLRGKQVGS 158  
 QY 70 LPEYTT-----RKRRGGQGFISQSEVNITQGMSSNNTYGVKNGNSIF-EDSSRKCA 123  
 DB 159 --GVTTDQVQAKKEGSPPTTKVSTLTIKEDMWSQSFTRGVHRLGTLFQNMSSMCV 216  
 QY 124 DSNPRGVSAYLSRSPFDLPIKSPPTTGLVVDLAPSKCTVNLWTSRPSGKPVNSTRKE 183  
 DB 217 PDODTARVFAIPSPFASIFLTKSTLTCLVVDLT-TYDSVITSWTRONGEAVKHTNIS 275  
 QY 184 EKQNGNGLVYVSTLPVGTGDMTEGTYQCRVTHPHLPRALMRSTKRLPKGL-AREVYWL 242  
 DB 276 ESHPNATFSVAGASICEDDNGSERFTCTVHTHDLPSLKQITRPRGVALLHRDVIIL 335  
 QY 243 PPSPEBTG--TTRVTCLIRGYSSEISVQWTFNNEBDHTGHTTTPQKHGTDPSFLL 300  
 DB 336 PPARQQLNRESATITCLTGVSPADVFQVMQRCQPLSPKRYTSAPWEPQADGRYFA 395  
 QY 301 YSRMLVNSKSIWKGNIYTCRVVHVALPG---SRITLKS 335  
 DB 396 HSLITVSSSRMTGSEYTYTCVVAHEALPNRYTERIVDKS 433  
 RESULT 10  
 MUC\_MOUSE STANDARD; PRT; 455 AA.  
 AC P01872;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE IG mu chain C region secreted form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81076590; PubMed=6255422;



RA Kawakami T., Takahashi N., Honjo T.;  
 RT "Complete nucleotide sequence of mouse immunoglobulin mu gene and  
 RT comparison with other immunoglobulin heavy chain genes."; *Nucleic Acids Res.* 8:3933-3945(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82051295; PubMed=6795090;  
 RA Goldberg G.I., Vanin E.F., Zrolka A.M., Blattner F.R.;  
 RT "Sequence of the gene for the constant region of the mu chain of  
 RT Balb/c mouse immunoglobulin."; *Gene* 15:33-42(1981).  
 RN [3]  
 RP SEQUENCE FROM N.A. (MYELOMA TEPCL183).  
 RX MEDLINE=81165562; PubMed=6260591;  
 RA Auffray C., Rougeon P.;  
 RT "Nucleotide sequence of a cloned cDNA corresponding to secreted mu  
 RT chain of mouse immunoglobulin."; *Gene* 12:77-86(1980).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 104E).  
 RX MEDLINE=79223904; PubMed=111247;  
 RA Kehy M.R., Sibley C.H., Fuhrman J.S., Schilling J.W., Hood L.E.;  
 RT "Amino acid sequence of a mouse immunoglobulin mu chain."; *Proc. Natl. Acad. Sci. U.S.A.* 76:2932-2936(1979).  
 RN [5]  
 RP REVISION (MOPC 104E).  
 RX MEDLINE=83075344; PubMed=6816276;  
 RA Kehy M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,  
 RT Hood L.E.;  
 RT "Complete amino acid sequence of a mouse mu chain: homology among  
 RT heavy chain constant region domains."; *Biochemistry* 21:5415-5424(1982).  
 RN -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=During differentiation, B lymphocytes switch from  
 CC expression of isoform Membrane-bound to isoform Secreted;  
 CC Name=Secreted;  
 CC IsoId=PI01872-1; Sequence=Displayed;  
 CC Name=Membrane-bound;  
 CC IsoId=PI01873-1; Sequence=External;  
 CC -----  
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 CC -----  
 CC EMBL; V00827; -; NOT\_ANNOTATED\_CDS.  
 DR DR PIR; A02166; MEMS.  
 DR HSSP; P01857; 1FCL.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MEC.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00407; IgC1; 2.  
 DR PROSITE; PS00835; IG LIKE; 4.  
 DR PROSITE; PS00290; IG\_MEC; 3.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing.  
 FT NON\_TER 1  
 FT DOMAIN 1  
 FT DOMAIN 105  
 FT DOMAIN 106  
 FT DOMAIN 217  
 FT DOMAIN 218  
 FT DOMAIN 324  
 FT DOMAIN 325  
 FT DOMAIN 436  
 FT DOMAIN 437  
 FT DOMAIN 455  
 FT DISULFID 14  
 FT DISULFID 14  
 FT DISULFID 28  
 FT DISULFID 89  
 FT DISULFID 136  
 FT DISULFID 199  
 FT DISULFID 216  
 FT DISULFID 305  
 FT DISULFID 246

FT DISULFID 293  
 FT DISULFID 353  
 FT DISULFID 454  
 FT DISULFID 454  
 FT CARBOHYD 46  
 FT CARBOHYD 211  
 FT CARBOHYD 211  
 FT CARBOHYD 243  
 FT CARBOHYD 281  
 FT CARBOHYD 281  
 FT CARBOHYD 442  
 FT CARBOHYD 442  
 FT CARBOHYD 78  
 FT CARBOHYD 101  
 FT CARBOHYD 101  
 FT CARBOHYD 226  
 FT CARBOHYD 226  
 FT CARBOHYD 258  
 FT CARBOHYD 258  
 FT CARBOHYD 368  
 FT CARBOHYD 368  
 FT CARBOHYD 455 AA; 50101 MW; 4CB857CB602F9B51 CRC64;  
 SO SEQUENCE  
 Query Match 25.3%; Score 469; DB 1; Length 455;  
 Best Local Similarity 34.1%; Pred. No. 9, 4e-29;  
 Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;  
 QY 23 PTYKLFHSSCDPR---GDASTIQQLCLVSGFSPAKYVWLVQDAENLF---PYTT 75  
 DB 112 PNVNVF---VPRDGRSGAPRKSRLICENTFTPRPIVSWLKQKLVESGFTTDPVTI 168  
 QY 76 RPRREGGQTPSLQSEVNTTQGMMSNTTTCYKANGSIF-EDSRKCADSNPRGVSAVL 134  
 DB 169 ENKSTPTQYKXVSTLTISEIDMLNVTYCVDRHGLFLKNVSTCAASPTDILPT 228  
 QY 135 SRSPFDLFIKSPPTTCVLDLAPSKGVNTLWRSAGKPNVHSTRKEKRNGLTVT 194  
 DB 229 IPRSFADILSKSANLCLVSNLATE-ILNLSMSQSEPELETIKIMESHPNGFSK 287  
 QY 195 STLPVGTQWISGEYQCYVTHPLPALMRSTYKLPK-RLADPVMLPSPSESTG-- 250  
 DB 288 GVAACVCEVMNNRKEVCVTRHDLPSQKFIK-PNVHNGPPAVYLLPARBQLNR 346  
 QY 251 TTRVTCILRGFSPHSISYOWLNNEDHTGHHTTRPKDHTGSPFLYSRLVYKSI 310  
 DB 347 ESNVTCVVKSGSPADISYQLRGQLPQEKYVTSAPPEVAGFGYTHILVTEEE 406  
 QY 311 WERKNLVTCRVYHEALP---GSRLEKS 335  
 DB 407 WNGEYTCVWGHEALPHLVTRTVDKS 434  
 RESULT 11  
 MUCM\_MOUSE STANDARD; PRT; 476 AA.  
 AC P01873;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ig mu chain C region membrane-bound form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE OF 433-476 FROM N.A.  
 RX MEDLINE=80222874; PubMed=6771020;  
 RA Early P., Rogers J., Davis M., Calame K., Bond M., Wall R.,  
 RT Hood L.;  
 RT "Two mRNAs can be produced from a single immunoglobulin mu gene by  
 RT alternative RNA processing pathways."; *Cell* 20:313-319(1980).  
 RN [2]  
 RP SEQUENCE OF 410-476 FROM N.A. (MYELOMA MOPC 104E).  
 RX MEDLINE=80222873; PubMed=6771019;  
 RA Rogers J., Early P., Carter C., Calame K., Bond M., Hood L.,  
 RT Wall R.;  
 RT "Two mRNAs with different 3' ends encode membrane-bound and secreted  
 RT forms of immunoglobulin mu chain."; *Cell* 20:303-312(1980).

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CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=During differentiation, B lymphocytes switch from
CC expression of isoform Membrane-bound to isoform Secreted;
CC Name=Membrane-bound;
CC IsoId=P01873-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01872-1; Sequence=External;
CC -!- MISCELLANEOUS: The sequence of residues 1-409 is assumed to be
CC identical with the corresponding region of the secreted form.
CC -----
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CC -----
DR EMBL: V00821; CA24202.1; -
DR PIR: A02167; MMSM.
DR HSSP: P01857; 1FC1.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_4.
DR SMART: SM00407; IGc1. 2.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
KW Alternative splicing; Transmembrane.
FT DOMAIN 1 105 CH1.
FT DOMAIN 106 217 CH2.
FT DOMAIN 218 324 CH3.
FT DOMAIN 325 436 CH4.
FT TRANSMEM 456 473 POTENTIAL.
FT DISULFID 14 14 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).
FT DISULFID 18 89
FT DISULFID 136 199 BY SIMILARITY.
FT DISULFID 216 216 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 246 305 BY SIMILARITY.
FT DISULFID 253 293 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
FT DISULFID 353 415 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 476 AA; 52656 MW; 8D476575A5204071 CRC64;

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## Query Match

25.3%; Score 469; DB 1; Length 476;  
 Best Local Similarity 34.1%; Pred. No. 9, 9e-29;  
 Matches 112; Conservative 57; Mismatches 139; Indels 20; Gaps 9;

```

QY 23 PTVKLFHSSCDPR---GDAHSTIOLCLVSGFSPAKVHTVLVDGQAEALNF---PPTT 75
DB 112 PAVNVF---VPRDGGSPAPRKSKLICEAINFTKPTVSWLNDGKAVESGFTTDPYTI 168
QY 76 RPKREGQTFSLQSEVNIITQOGMSSNTYTCVKNKNSIF-EDSSRKCADSNPRGSAVL 134
DB 169 ENKSGPTQYKVIISTLTISEIDMLNLYTCVDRGLTFLKNVSGTCAASPSTDLFT 228
QY 135 SPSPPDLFIKSPPTTCLVLDLAPSKGVNLTWSRASKPVNSTRKEEQKQRTLVY 194
DB 229 ITPSPADIFLSKSNITCLVSNLAYE-TLNTSMAQSEPLETIKIMESHNPSTFAK 287
QY 195 STLPVGRDMIGETVQCRVTHPHLPALMRSTKLPGK--RLAEVYMLPPSPERTG-- 250
DB 288 GVAASVEEDMNRKEFCVTRHDLPSPOKFKISK-PNEVHGHPAVYLLPARRQNLAR 346
QY 251 TTRTVYCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFLVSRMLYKSI 310
DB 347 ESATVYCLVKGSPADISVQWLOKQLLPQEKYVTSAPPEPGADGFYTHSILTVTEE 406

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QY 311 WEKGNLVTCRVVHEALP---GSRITLKS 335
DB 407 WNSGERTCVVGHREALPHLYTERTYDKS 434

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## RESULT 12

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ID MCB_HUMAN STANDARD; PRT; 391 AA.
AC P04220;
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig mu heavy chain disease protein (BOT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=64184186; PubMed=6425189;
RA Barnikol-Watanabe S., Mhaesco E., Mhaesco C., Barnikol H.U.,
RA Hilschmann N.;
RT "The primary structure of mu-chain-disease protein BOT. Peculiar
RT amino-acid sequence of the N-terminal 42 positions.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
CC -!- MISCELLANEOUS: This protein has no V region homology or CH1
CC region.
DR PIR: A02163; MHUBT.
DR HSSP: P01857; 1FC1.
DR GO: GO:0005624; C:membrane fraction; NAS.
DR GO: GO:0003823; P:antigen binding; TAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_4.
DR SMART: SM00407; IGc1. 2.
DR PROSITE: PS50835; IG_LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
KW FRB-C-Part (NO V REGION HOMOLOG).
FT DOMAIN 1 42
FT DOMAIN 43 155 CH2.
FT DOMAIN 156 261 CH3.
FT DOMAIN 262 391 CH4.
SQ SEQUENCE 391 AA; 43057 MW; 9100843AFC021A CRC64;

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## Query Match

24.8%; Score 460; DB 1; Length 391;  
 Best Local Similarity 31.1%; Pred. No. 3, 8e-28;  
 Matches 105; Conservative 64; Mismatches 145; Indels 24; Gaps 11;

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QY 15 SGVYTI-IPPTVYLFHSSCDPR---GDAHSTIOLCLVSGFSPAKVHTVLVDGQAEALNF---PPTT 75
DB 40 SGPVIALPDKPVSVF---VPRDGGSPAPRKSKLICEAINFTKPTVSWLNDGKAVESGFTTDPYTI 168
QY 70 LFPYTT-----RPRKREGQTFSLQSEVNIITQOGMSSNTYTCVKNKNSIF-EDSSRKA 123
DB 96 -GVTTDEVAEAKESGPTTYKVTSTLTIKESDWMQGSNFTCRVDRGLTFLKNVSGTCAASPSTDLFT 228
QY 124 DSNPRGSAVLSRPSPPDLFIKSPPTTCLVLDLAPSKGVNLTWSRASKPVNSTRKEEQKQRTLVY 194
DB 154 PDQDTAIRFALIPSPASIFLTKSTKLTCLVLDL-TYDSVITISWTRDQGEAVKHTNIS 212
QY 184 EKQKNGTLVYSTLPVGRDMIGETVQCRVTHPHLPALMRSTKLPGK--RLAEVYMLPPSPERTG-- 250
DB 213 ESHPNATFAVAGASICEDWDGSEKFTCVHTHDLPSFLKQITIRPKGVALLHRDVAVL 272
QY 243 PPSPEERTG--TTRTVYCLIRGFYPSISVQWLFNNEEDHTGHTTTRPOKHGTDPSFLVSRMLYKSI 310
DB 273 PPARBQLNLRASATITCLVTFSPADVFQWQMRGQPSPEKYVTSAPPEPGADGFYTHSILTVTEE 406
QY 301 YSRMLYKSIWEKGNLVTCRVVHEALP---GSRITLKS 335

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DB 333 HSILFTVSEEMNTGETYTCVAHEALPNKVERTYDKS 370

RESULT 13  
 ID\_GCL\_HUMAN STANDARD; PRT; 330 AA.  
 AC P01857;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE IG gamma-1 chain C region.  
 GN IGHG1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=82274238; PubMed=6287432;  
 RA Ellison J.W., Berson B.D., Hood L.E.;  
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
 RL Nucleic Acids Res. 10:4071-4079(1982).  
 RN [2]  
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
 RX MEDLINE=71064024; PubMed=5489771;  
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
 RT Wexler M.U., Edelman G.M.;  
 RL "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
 RN Biochemistry 9:3161-3170(1970).  
 RN [3]  
 RP SEQUENCE OF 136-329 (EU).  
 RX MEDLINE=71064025; PubMed=5530842;  
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.;  
 RT Edelman G.M.;  
 RL "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
 RN Biochemistry 9:3171-3181(1970).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN NIE).  
 RX MEDLINE=77070269; PubMed=826475;  
 RA Fostling H., Hilschmann N.;  
 RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
 RN [5]  
 RP SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.  
 RX MEDLINE=83289131; PubMed=6884994;  
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
 RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
 RN [6]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=71064027; PubMed=4923144;  
 RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 RN [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=77070267; PubMed=1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;

RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the GIM(1) marker, 239-D and 241-L. KOL and EU sequences have the GIM(3) marker and the GIM (non-1) markers.  
 CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35, 116, 198, 269 and 272.  
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 198, 269, and 272 and in the order of residues 268-272.  
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.  
 CC -----  
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 CC -----  
 DR EMBL; U00228; AAC82527.1; AUT\_INIT.  
 DR PIR; A93433; GHHD.  
 DR PDB; 1FC1; 15-JUL-92.  
 DR PDB; 1FC2; 15-JUL-92.  
 DR PDB; 1A77; 12-NOV-97.  
 DR PDB; 1D58; 09-FEB-00.  
 DR PDB; 1D57; 09-FEB-00.  
 DR PDB; 1D6V; 04-OCT-00.  
 DR PDB; 1DN2; 17-MAY-00.  
 DR PDB; 1B4K; 06-JUN-01.  
 DR PDB; 1FCC; 20-JUL-95.  
 DR PDB; 1H2H; 12-JUN-02.  
 DR PDB; 1I7Z; 08-AUG-01.  
 DR PDB; 1I7S; 16-MAY-01.  
 DR PDB; 1I7K; 16-MAY-01.  
 DR PDB; 1L6X; 10-APR-02.  
 DR PDB; 2RCS; 12-NOV-97.  
 DR Genew; HGNC:5525; IGHG1.  
 DR MIM; 147100; -.  
 DR GO; GO:0005624; C-membrane fraction; NAS.  
 DR GO; GO:0003823; F-antigen binding; NAS.  
 DR GO; GO:0006955; P-immune response; NAS.  
 DR Interpro; IPR007110; Ig-like.  
 DR Interpro; IPR003597; Ig\_Like.  
 DR Pfam; PF00047; Ig\_3.  
 DR SMART; SM00407; IgG1; 2.  
 DR PROSITE; PSS0835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW 3D-structure.  
 FT PT NON TER 1 1  
 FT PT DOMAIN 1 98  
 FT PT DOMAIN 99 110  
 FT PT DOMAIN 111 223  
 FT PT DOMAIN 224 330  
 FT PT DISULFID 227 83  
 FT PT DISULFID 103 103  
 FT PT DISULFID 109 109  
 FT PT DISULFID 112 112  
 FT PT DISULFID 144 204  
 FT PT DISULFID 250 308  
 FT PT CARBOHYD 180 180  
 FT MOD RES 330 330  
 FT VARIANT 97 97  
 FT VARIANT 239 239  
 FT VARIANT 241 241  
 FT VARIANT 241 241  
 N-LINKED (GLNAC. . .).  
 REMOVED POST-TRANSLATIONALLY.  
 K -> R (IN GIM(3) MARKER).  
 D -> E (IN GIM(NON-1) MARKER).  
 /FTID=VAR 003886.  
 L -> M (IN GIM(NON-1) MARKER).

FT STRAND 122 126 /FTID=VAR\_003888.  
 FT HELIX 130 134  
 FT TURN 136 137  
 FT STRAND 141 147  
 FT STRAND 157 162  
 FT TURN 163 164  
 FT STRAND 165 166  
 FT TURN 168 171  
 FT STRAND 176 179  
 FT TURN 180 181  
 FT STRAND 182 190  
 FT HELIX 193 197  
 FT TURN 198 199  
 FT STRAND 202 207  
 FT TURN 209 210  
 FT STRAND 215 219  
 FT STRAND 227 229  
 FT STRAND 230 234  
 FT HELIX 238 242  
 FT STRAND 245 256  
 FT STRAND 260 265  
 FT STRAND 270 276  
 FT STRAND 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 305 312  
 FT TURN 313 314  
 FT TURN 316 317  
 FT STRAND 320 325  
 SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2F933D CRC64;

Query Match 24.5%; Score 454; DB 1; Length 330;  
 Best Local Similarity 34.4%; Pred. No. 9e-28;  
 Matches 117; Conservative 57; Mismatches 130; Indels 36; Gaps 12;

QY 22 PPTVYKLFHSSCDPRGHAHTIOLCLVSGSPAKHYWYV---LYDQGAENLFPYITRP 77  
 DB 6 PSYFPIAPSSKSTSG--GTAALGCLVQDYFPEPTVWMSGALTSG--VHTPEAVL-- 57  
 QY 78 KREGGQTFSLQSEVNTTQGWMSNTYTCHVKNHSIFE-----DSRRC---A 123  
 DB 58 --QSSGLYSLSSVTVPSSS--LGOTYICNVNKHPSNPKVKYKPEKSCDKHTCCPCPA 114  
 QY 124 DSNPDSVAVLSRPSFD-LFTRKSPITTCVVDLAPKGVNLTWSASGKPYNHSRTR 182  
 DB 115 PELLGGPSVFLPPPKXDTLMSKTPVETCVVDVSHEDPEYKFMVYDGVENAKTKP 174  
 QY 183 EERKONGTLVTSTLPVGTDMIEGETYQCRVTHPLPALMRSTTKLPGKRLAPEVYM 242  
 DB 175 REQVNSTVAVSVLVTHQDWLNGKEYCKVSNALPAPLEKITSKAKGPREPQVYTL 234  
 QY 243 PPSPEE-TGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTRPKQKHGTPSPFELY 301  
 DB 235 PPRDELTKQVSLTCLVKGFTPSDLAVHMSNGPEN--NYKTTTPVLD--SDGSFELY 290  
 QY 302 SRMLVANKSIWEKGNLVTQCVVHEALPGSRTEKSLHYSAG 341  
 DB 291 SKLTVDKSRWQGNVPSGVMEHALHNHT--OKSLTSLSPG 329

RESULT 14  
 MUC\_SUMMU  
 ID\_MUC\_SUMMU STANDARD; PRT; 457 AA.  
 AC P20768;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 1g mu chain C region.  
 OS Suncus murinus (House shrew). (Musk shrew).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.  
 OC NCBI\_TaxID=9378;  
 (1)  
 RC TISSUE=Liver;  
 RC MEDLINE=89232144; PubMed=2497033;  
 RA Ishiguro H., Ichihara Y., Nankawa T., Nagatsu T., Kurosawa Y.;  
 RT "Nucleotide sequence of Suncus murinus immunoglobulin mu gene and  
 RT comparison with mouse and human mu genes";  
 RL FEBS Lett. 247:317-322(1989).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, X13920; CAA32113.1; ALT\_INIT.  
 DR PIR; S03961; S03961.  
 DR HSP; P01842; 7EAB.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00407; IgC1; 3.  
 DR PROSITE; PS50835; Ig LIKE; 4.  
 DR PROSITE; PS00290; Ig\_MHC; 3.  
 KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 105 CH1.  
 FT DOMAIN 106 220 CH2.  
 FT DOMAIN 221 326 CH3.  
 FT DOMAIN 327 457 CH4.  
 FT DISULFID 13 13 INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE).  
 FT DISULFID 27 89 BY SIMILARITY.  
 FT DISULFID 136 200 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT DISULFID 217 217 BY SIMILARITY.  
 FT DISULFID 248 307 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT DISULFID 295 295 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT DISULFID 355 417 BY SIMILARITY.  
 FT DISULFID 456 456 INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).  
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 457 AA; 50074 MW; 56C8C086DA46289 CRC64;

Query Match 24.2%; Score 450; DB 1; Length 457;  
 Best Local Similarity 31.2%; Pred. No. 2.7e-27;  
 Matches 105; Conservative 67; Mismatches 142; Indels 22; Gaps 9;

QY 21 IPTVYKLFHSSCDPRGHAHTIOLCLVSGSPAKHYWYV---LYDQGAENLFPYITRP 75  
 DB 110 LPNVSIF--VPRNSPSGNHPTSQLQASGFSRTVWMLRGEGVQSGVSYSA 166  
 QY 76 --RPRKGGQTFSLQSEVNTTQGWMSNTYTCHVKNHSIFE--SSRKCADSNPAGV 130  
 DB 167 VEABPKSGSPTTFRAVIRLITTEBMLSGREFCOALHKLFTQKNVSVQWMDDTSTGI 226  
 QY 131 SAYLSRPSFDLFTKSPITTCVVDLAPKGVNLTWSASGKPYNHSRTRKEXRNGT 190  
 DB 227 SVFLPPTFANIFITQSAQLTCLVTA--TYSDLSWSKQNEALQTVNISESPNST 285  
 QY 191 LVTSTLPVGTDMIEGETYQCRVTHPLPALMRSTTKLPGKRLA--PEVYMLPSPSE 247  
 DB 286 FTAKGASVCSEWESEKFTCTVQSHDLSPKQHSR--PCVANDPPSVFVLPAGE 343  
 QY 248 E--TGTRTVTCLIRGFYPSSEISVQWLFNNEEDHTGHTTRPKQKHGTPSPFELYRML 305

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Db 344 QLKRESASITCLVKDPSPPDVFWQHQHQPDPDPKHVYTSNTPPPQNGLYFVSIILT 403
QY 306 VNKSIEWKGNLVTCRVVHEALPGSRITLKSILHSAG 341
Db 404 VSEKDWSSGESFSFCVVGHEALPLSVT-EKAVDKTSG 438
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## RESULT 15

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MUC_CANFA
ID MUC_CANFA STANDARD; PRT; 450 AA.
AC P01874;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG mu chain C region.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE OF 1-177 (MOO).
RX MEDLINE=80077682; PubMed=117299;
RA "McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
RN [2]
RP SEQUENCE OF 178-450 (MOO).
RX MEDLINE=78180587; PubMed=653360;
RA Wasserman R.L., Capra J.D.;
RT "Amino acid sequence of the Fc region of a canine immunoglobulin M:
RT interpectes homology for the IgM class.";
RL Science 200:1159-1161(1978).
DR PIR; A93131; MHDG.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGH; 2.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON TER
SQ SEQUENCE 450 AA; 48895 MM; 9D460DA9D1012F5D CRC64;
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Query Match 23.9%; Score 444; DB 1; Length 450;  
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QY 67 AENLPPTYT-----RPRREGQTFSLQSEVNITQGMSSNTYTCVKNENGSTP-EDSGR 120
Db 152 IES--GYTTVEVZAAZASZSGPTTYKVTSMLTQEDAWLSQVFCVKEHRLGTLFOONASS 209
QY 121 KCADSNRGVSAYLSRPSPPDLFIRKSPITICLVVDLAPSKGVNLTWMSRASGKPVNHST 180
Db 210 MCTSDQPGVIGISITFIPSPFASIFNTKSAKLSCLVTDLA-TYDSYTSITRENGALKTHT 268
QY 181 RKEEKQNGTLVTSTLPVGRDWIEGETYQCRVTHPLPALMRSTTKLPGRKL-APEY 239
Db 269 NISSEHPGTFPSAMGEATVCEWEESGQFCTVTHDLPSTVLKQTSRPGVAVHWPSTV 328
QY 240 YMLPSPPEPTG--TTRVTYCLIRGFYSEISVQWLNNNEBDHTGHTTTRPQKHGTDPS 297
Db 329 YVLPSPREQLDLRESATISCLVYGSPPDVFWQVQKQPPPPSYTSAIPMEPQAPGL 388
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Db 389 YFAHSILTVSEEWNAGETYTCVVAHSLP-NRYTFRSVDKSTG 431
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Search completed: February 26, 2004, 11:59:20  
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: February 26, 2004, 11:45:31 ; Search time 20 Seconds  
(without alignment)  
1644.875 Million cell updates/sec

Title: US-09-401-636-8  
Perfect score: 1856  
Sequence: 1 EFHHHHHTSLPESGPVTL.....HEALPGSRLEKSLHYSAGN 342

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
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2	1024.5	55.2	426	2 I36948	Ig epsilon chain C
3	767.5	41.4	429	1 EHRT	Ig epsilon chain C
4	751	40.5	388	1 EHNS	Ig epsilon chain C
5	682	36.7	548	2 S38864	Ig epsilon chain C
6	673	36.3	423	1 EHMS	Ig epsilon chain C
7	580.5	31.3	572	2 B46529	Ig epsilon chain C
8	535.5	28.9	504	2 S00390	Ig epsilon chain C
9	497.5	26.8	479	1 MHRBM	Ig epsilon chain C
10	496	26.7	454	1 MHRB	Ig epsilon chain C
11	495.5	26.7	458	1 MHRB	Ig epsilon chain C
12	486.5	26.2	326	1 G2HU	Ig epsilon chain C
13	480.5	25.9	343	2 S25644	Ig epsilon chain C
14	476	25.6	327	1 G4HU	Ig epsilon chain C
15	475.5	25.6	627	2 S14683	Ig epsilon chain C
16	473.5	25.5	328	2 I41161	Ig epsilon chain C
17	472	25.4	433	2 S31436	Ig epsilon chain C
18	469	25.3	455	1 MHRB	Ig epsilon chain C
19	469	25.3	455	2 A24976	Ig epsilon chain C
20	469	25.3	476	1 MHRB	Ig epsilon chain C
21	468	25.2	328	2 I41160	Ig epsilon chain C
22	465	25.1	328	2 I41159	Ig epsilon chain C
23	465	25.1	453	2 S37768	Ig epsilon chain C
24	465	25.1	453	2 S15590	Ig epsilon chain C
25	463.5	25.0	328	2 I41158	Ig epsilon chain C
26	460	24.8	391	1 MHRB	Ig epsilon chain C
27	458.5	24.7	592	2 S25705	Ig epsilon chain C
28	454	24.5	330	1 GHRU	Ig epsilon chain C
29	453.5	24.4	452	1 MHRU	Ig epsilon chain C

30	453.5	24.4	473	1 MHRUM	Ig mu chain C regi
31	450	24.2	457	2 S03961	Ig mu chain C regi
32	447	24.1	277	2 I47162	Ig gamma-1 chain C
33	447	24.1	377	2 A60764	Ig gamma-3 chain C
34	447	24.1	377	2 A23511	Ig gamma-3 chain C
35	446.5	24.1	374	2 S69339	Ig heavy chain V r
36	444	23.9	450	1 MHDG	Ig mu chain C regi
37	443.5	23.9	322	2 PS0019	Ig gamma-2a chain
38	440	23.7	472	2 S11459	Ig gamma-1 chain C
39	437.5	23.6	323	1 GHRB	Ig gamma chain C r
40	437.5	23.6	444	2 PC4436	monoclonal antibod
41	436.5	23.5	326	2 PS0017	Ig gamma-1 chain C
42	429	23.1	470	2 S22080	Ig heavy chain pre
43	428	23.1	329	2 S00847	Ig gamma-2c chain
44	428	23.1	549	2 S04845	Ig heavy chain pre
45	424.5	22.9	329	1 G2GP	Ig gamma-2 chain C

## ALIGNMENTS

RESULT 1  
EHHU  
Ig epsilon chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1981 #sequence\_revision 13-Jun-1983 #text\_change 16-Jul-1999  
C/Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46  
R/Planagan, J.G.; Rabbitt, T.H.  
EMBO J. 1, 655-660, 1982  
A/Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene  
A/Reference number: A22771; MUID:84236029; PMID:6234164  
A/Accession: A22771  
A/Molecule type: DNA  
A/Residues: 1-428 <FLA>  
A/Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:G185035  
R/Ueda, S.; Nakai, S.; Nishida, Y.; Hiseajima, H.; Honjo, T.  
EMBO J. 1, 1539-1544, 1982  
A/Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog  
A/Reference number: A23195; MUID:84207910; PMID:6327276  
A/Accession: A23195  
A/Molecule type: DNA  
A/Residues: 2-428 <UED>  
A/Cross-references: GB:J00222; NID:G184755  
R/Zhang, K.; Saxon, A.; Max, E.E.  
J. Exp. Med. 176, 223-243, 1992  
A/Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing  
A/Reference number: PH1214; MUID:92308839; PMID:1613458  
A/Accession: PH1214  
A/Molecule type: DNA  
A/Residues: 320-428 <ZHA>  
A/Cross-references: EMBL:X63693; GB:S38668; NID:G32987  
R/Seno, M.; Kurokawa, T.; Ono, Y.; Ono, H.; Saesada, R.; Igarashi, K.; Kikuchi, M.; Sugii  
Nucleic Acids Res. 11, 719-726, 1983  
A/Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha  
A/Reference number: A93491; MUID:83168897; PMID:6300763  
A/Accession: A93491  
A/Molecule type: mRNA  
A/Residues: 1-428 <SEN>  
A/Cross-references: GB:I00022; GB:J00227; GB:V00555; NID:G185035  
R/Mex, E.E.; Batey, J.; Ney, R.; Kirsch, I.R.; Leder, P.  
Cell 29, 691-699, 1982  
A/Title: Duplication and deletion in the human immunoglobulin epsilon genes.  
A/Reference number: A90824; MUID:83001945; PMID:6288268  
A/Accession: A90824  
A/Molecule type: DNA  
A/Residues: 1-358, 1', 360-428 <MAX>  
A/Cross-references: GB:J00222; NID:G184755  
R/Bennich, H.H.; Johansson, S.G.O.; Von Bahrt-Undstrom, H.  
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3  
A/Reference number: A94418  
A/Accession: A94418  
A/Molecule type: protein

A:Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12  
 A:Experimental source: myeloma protein Nd  
 R:Kanten, J.H.; Mølgård, H.V.; Houghon, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982  
 A:Title: Cloning and sequence determination of the gene for the human immunoglobulin eps  
 A:Reference number: A53933; MUID:83065234; PMID:6815656  
 A:Accession: B39333  
 A:Molecule type: mRNA  
 A:Residues: 1-40;68-114;427-428 <KEN>  
 A:Cross-references: GB:100022; NID:G185035  
 R:Ikeyama, S.  
 FEBS Lett. 224, 306-310, 1987  
 A:Title: Purification and characterization of a recombinant human Ige Fc-epsilon fragment  
 A:Reference number: S02438; MUID:88083554; PMID:3121387  
 A:Accession: S02438  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 98-352 <IKE>  
 R:Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.  
 J. Biol. Chem. 269, 456-462, 1994  
 A:Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces  
 A:Reference number: A53116; MUID:94103254; PMID:8276835  
 A:Accession: A53116  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 320-428 <ZH2>  
 A:Experimental source: myeloma U266-derived cell line AF-10  
 A:Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBI:141702)  
 R:Hellman, L.  
 Eur. J. Immunol. 23, 159-167, 1993  
 A:Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of  
 A:Reference number: A46536; MUID:93122085; PMID:8419166  
 A:Accession: C46536  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 382-426 <HEL>  
 A:Cross-references: GB:S55273; NID:G263166; PIDN:AA24857.1; PID:G263167  
 A:Experimental source: B cell myeloma U-266  
 A:Note: sequence extracted from NCBI backbone (NCBIP:125297)  
 A:Accession: D46536  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 382-391 <HE2>  
 A:Cross-references: GB:S55276; NID:G263168; PIDN:AA24858.1; PID:G263169  
 A:Experimental source: B cell myeloma U-266  
 A:Note: sequence extracted from NCBI backbone (NCBIP:125299)  
 A:Accession: A46536  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 401-428 <HE3>  
 A:Cross-references: GB:S53497; NID:G263162; PIDN:AA24855.1; PID:G263163  
 A:Experimental source: B cell myeloma U-266  
 A:Note: sequence extracted from NCBI backbone (NCBIP:123483)  
 C:Genetics:  
 A:Gene: GDB:IGHE  
 A:Cross-references: GDB:119335; OMIM:147180  
 A:Map position: 14q32.33-14q32.33  
 A:Intron: 1/1; 104/1; 211/1; 319/1  
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin  
 F:128-87/Domain: immunoglobulin homology <IM1>  
 F:128-195/Domain: immunoglobulin homology <IM2>  
 F:232-301/Domain: immunoglobulin homology <IM3>  
 F:338-407/Domain: immunoglobulin homology <IM4>  
 F:4/Disulfide bonds: interchain (to light chain) #status predicted  
 F:15-105,29-85,135-193,239-299,345-405/Disulfide bonds: #status predicted  
 F:11,49,59,146,252,275/Binding site: carbohydrate (Asn) #status experimental  
 F:121,209/Disulfide bonds: interchain (to heavy chain) #status predicted

Query Match 56.0%; Score 1038.5; DB 1; Length 428;  
 Best Local Similarity 62.4%; Pred. No. 9.9e-71;

Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;  
 QY 22 PPTVTKLFHSSCDPRGAAHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 81  
 DB 111 PPTVTKLFHSSCDPRGAAHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 168  
 QY 82 GQTFSLQSEVNIITQGMMSNTYTCVKANGSIPEDSRKCADSNRGVSAVLSRSPFD 141  
 DB 169 GELASTQSELTLSQKMWLSDRITTCQVYQGHFPESTKCADSNRGVSAVLSRSPFD 228  
 QY 142 LPIKSPITTCVVDLAPSGKTVNLWTSRSGKPVNHSRKEKQNGTLVTSLPVGT 201  
 DB 229 LPIKSPITTCVVDLAPSGKTVNLWTSRSGKPVNHSRKEKQNGTLVTSLPVGT 288  
 QY 202 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 259  
 DB 289 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 347  
 QY 260 RGFYPSISVQMLFNNEEDHTGHTTRPOKHGTDPSEFLYSRMLVNSIWEKGNLYTC 319  
 DB 348 QNFVPEISVQMLFNNEEDHTGHTTRPOKHGTDPSEFLYSRMLVNSIWEKGNLYTC 405  
 QY 320 RVVHEALPGSRTEKSLHYSAG 341  
 DB 406 RVVHEALPGSRTEKSLHYSAG 427  
 RESULT 2  
 136948  
 Ige epsilon-chain - chimpanzee (fragment)  
 C:Species: Pan troglodytes (chimpanzee)  
 C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jan-2000  
 C:Accession: 136948  
 R:Sakoyama, Y.; Hong, K.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987  
 A:Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangute  
 A:Reference number: 136948; MUID:87147136; PMID:3103123  
 A:Accession: 136948  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-426 <RES>  
 A:Cross-references: GB:M15398; NID:G176797; PIDN:AAA35416.1; PID:G176798  
 C:Genetics:  
 A:Introns: 103/1; 209/1; 317/1  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:338-405/Domain: immunoglobulin homology <IM1>  
 Query Match 55.2%; Score 1024.5; DB 2; Length 426;  
 Best Local Similarity 61.7%; Pred. No. 1.1e-69;  
 Matches 198; Conservative 42; Mismatches 74; Indels 7; Gaps 4;  
 QY 23 PTVLTFHSSCDPRGAAHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 82  
 DB 110 PTVLTFHSSCDPRGAAHSTIOLCLVSGFSPAKVHTVLVDQEAENLFPYTRPREKRG 167  
 QY 83 QTFSLQSEVNIITQGMMSNTYTCVKANGSIPEDSRKCADSNRGVSAVLSRSPFD 142  
 DB 168 GELASTQSELTLSQKMWLSDRITTCQVYQGHFPESTKCADSNRGVSAVLSRSPFD 227  
 QY 143 LPIKSPITTCVVDLAPSGKTVNLWTSRSGKPVNHSRKEKQNGTLVTSLPVGT 202  
 DB 229 LPIKSPITTCVVDLAPSGKTVNLWTSRSGKPVNHSRKEKQNGTLVTSLPVGT 287  
 QY 202 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 259  
 DB 289 RDMTGGTYQCRVTHPLPALMRSTTKLPGRKLAPVYMLPPSPETGT--TRVTCIL 346  
 QY 260 RGFYPSISVQMLFNNEEDHTGHTTRPOKHGTDPSEFLYSRMLVNSIWEKGNLYTC 319  
 DB 348 QNFVPEISVQMLFNNEEDHTGHTTRPOKHGTDPSEFLYSRMLVNSIWEKGNLYTC 404  
 QY 321 RVVHEALPGSRTEKSLHYSAG 341  
 DB 406 RVVHEALPGSRTEKSLHYSAG 427



Db 405 AVHEASPSQTVQRTVSVPNG 425

# RESULT 3

EHRT

IG epsilon chain C region - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 17-Dec-1982 #sequence\_revision 13-Jun-1983 #text\_change 16-Jul-1999

C/Accession: A93442; A90937; A02143  
R/Accession: A93442; A90937; A02143

R/Accession: A93442; A90937; A02143  
R/Accession: A93442; A90937; A02143

Nucleic Acids Res. 10, 6041-6049, 1982  
A/Title: Structure and evolution of the heavy chain from rat immunoglobulin E.

A/Reference number: A93442; MUID:83064537; PMID:6292865  
A/Accession: A93442

A/Molecule type: mRNA  
A/Residues: 1-429 <HEL>

A/Experimental source: Strain LOU/c/Mel, immunocytoma IR2  
R/Accession: A93442; A90937; A02143

A/Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, DNA 1, 335-343, 1982  
A/Reference number: A90937; MUID:83182019; PMID:6820340

A/Accession: A90937  
A/Accession: A90937

A/Molecule type: mRNA  
A/Residues: 1-169-307, 'L', 309-342 <KIN>

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F/19-80/Domain: immunoglobulin homology <IM1>

F/118-186/Domain: immunoglobulin homology <IM2>  
F/223-231/Domain: immunoglobulin homology <IM3>

F/327-398/Domain: immunoglobulin homology <IM4>  
F/46,99,170,240,265,369,419/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 41.4%; Score 767.5; DB 1; Length 429;  
Best Local Similarity 45.8%; Pred. No. 2,66-50;  
Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 4;

Db 17 PVTIIPPTVKLFHSCDPRGDAHSTIQLCVSGSPAKYVTVLVGQAEMLFPYTR 76

Db 97 PVTIIPPTVKLFHSCDPRGDAHSTIQLCVSGSPAKYVTVLVGQAEMLFPYTR 150

Db 77 PK----REGGQTFSLQSEVNTTQCGMSSNTYTCVKNHSIPEDSRKADSNPRGVA 132

Db 151 AQLVLIKEEGKLAATSRKNTTQCGMSSNTYTCVKNHSIPEDSRKADSNPRGVA 210

Db 133 YLSRSPSPDLFIRKSPITTCVVDLAPSKGTVNLWTSRAGKPVNSTRKEKQNGTLT 192

Db 211 YLIPSPDLIYENGTPKLTCLVLDL-ESEENITVTVREKKSIGSASQSTGKHATTS 269

Db 193 VTSLTPGTRMIGETTYQCVTHPHLPAALMRSTLQPKRLAPETVYMLPSPPEEGT 252

Db 270 ITSLPDAKMWISGEQVDPHPKPKVIRITAPGRSAPEVYVLPPEEEKDK 329

Db 253 RTVCLIRGEFYSISVQMLFNNEEDTGHHTTRPOKDKDTPSEFYLRLVNSIWE 312

Db 330 RTLCILQNFEPEDISVQWLDKILPKSQHSTTTPKYNQSGNRPFIPLREYALWT 389

Db 313 KGNLVTCRVVHEALPGSRTELEKSLHYSAQN 342

Db 390 QTKQFTCRVTHLEALREPKERTISKSLGN 419

# RESULT 4

EHMS

IG epsilon chain C region (version 1) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jun-1993 #sequence\_revision 13-Jun-1993 #text\_change 16-Jul-1999

C/Accession: A02144  
R/Accession: A02144

R/Accession: A02144  
R/Accession: A02144

A/Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A/Reference number: A02144; MUID:83117774; PMID:6818553

A/Accession: A02144  
A/Molecule type: mRNA

A/Residues: 1-388 <LTD>  
A/Cross-references: GB:J00476; NID:G194875; PID:AAA38085.1; PID:G387220

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F/1-44/Domain: immunoglobulin homology (fragment) <IM1>

F/81-149/Domain: immunoglobulin homology <IM2>  
F/186-254/Domain: immunoglobulin homology <IM3>

F/290-361/Domain: immunoglobulin homology <IM4>  
F/10,51,62,133,205,228,332,382/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 40.5%; Score 751; DB 1; Length 388;  
Best Local Similarity 44.8%; Pred. No. 4e-49;  
Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

Db 2 FHHHHHTLSLSPES-----GPVTIIPPTVKLFHSCDPRGDAHSTIQLCVSGSPAKV 56

Db 40 FCHVTHPPSFVESRTILVFPVNTIRPTLEHSSCDPNA-FHSTIQLCVGYHINDV 98

Db 57 HTVAVDQAEANLFPYTRRREGGQTFSLQSEVNTTQCGMSSNTYTCVKNHSGIFE 116

Db 99 SVSWMDREITDITLAQTVLKEE-GKLAATSRKNTTQCGMSSNTYTCVKNHSGIFE 157

Db 117 DSRKADSNPRGVAIYLRSPSPDLFIRKSPITTCVVDLAPSKGTVNLWTSRAGKPV 176

Db 158 AHTRCQPHRERGVTIYLPSPDLIYENGTPKLTCLVLDL-ESEENITVTVREKKSIGSASQSTGKHATTS 216

Db 177 NHSTRKEKQNGTLTSTLPVGTROMIIEBETTYQCVTHPHLPAALMRSTLQPKRLAPETVYMLPSPPEEGT 236

Db 217 SASQWTKHNNATTSITSIILPVAKMWISGEQVDPHPKPKVIRITAPGRSAPEVYVLPPEEEKDK 276

Db 237 PEVYVLPPEEEKDKRTITCLIQNFEPEDISVQWLDKILPKSQHSTTTPKYNQSGNRPFIPLREYALWT 296

Db 277 PEVYVLPPEEEKDKRTITCLIQNFEPEDISVQWLDKILPKSQHSTTTPKYNQSGNRPFIPLREYALWT 336

Db 297 SFELYSRLVNSIWEKGNLTVTCRVVHEALPGSRTELEKSLHYSAQN 342

Db 337 GFIFSRLEVAATLWTKQKQFTCVYHIALQPKRLAPETVYMLPSPPEEGT 382

RESULT 5  
IG epsilon chain C region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001

C/Accession: S38864  
R/Accession: S38864

R/Accession: S38864  
R/Accession: S38864

A/Status: preliminary  
A/Molecule type: mRNA

A/Residues: 1-548 <KIP>  
A/Cross-references: EMBL:227397; NID:G416537; PID:CAA1768.1; PID:G940782

C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F/353-421/Domain: immunoglobulin homology <IM1>

Query Match 36.7%; Score 682; DB 2; Length 548;  
Best Local Similarity 43.0%; Pred. No. 9.6e-44;  
Matches 142; Conservative 52; Mismatches 122; Indels 14; Gaps 4;

Db 12 LPESGPVTIIPPTVKLFHSCDPRGDAHSTIQLCVSGSPAKYVTVLVGQAEMLFPYTR 69

Db 229 VPEVSVTFIPPKXP-----DVTIRSTIQLCVGYHINDVSVSWMDREITD 278

Db 70 LFPYTRRREGGQTFSLQSEVNTTQCGMSSNTYTCVKNHSGIFE 129

Db 279 TLAQTVLKEE-GKLAATSRKNTTQCGMSSNTYTCVKNHSGIFE 337





Matches 118; Conservative 56; Mismatches 137; Indels 25; Gaps 10;

QY 17 PYTTPPTPKLPH--SSCDPRDASTITQLCLVSGSPAKVHTVNLVDGGAENLFFPTT 75  
 DB 172 FVPVAPAPVQVLAHSSCP--SOSSEVLLCLVGFSPASAEVMDG--VGLLVASQ 227  
 QY 76 RPKREGGQTFSLQSEVNTTQCGMMSNTYTCHVGH--NGSIFEDSRKADS-----NPRG 129  
 DB 228 SPARSGSTYLSLRVNVSGTDMREGKSYSCRVHPATNIVDEHVAGCGDGAQSCSP-- 285  
 QY 130 VSAVLSRSPFDLTIKRSPTTCLVVDLAPSKGTVNLTWSPASGKPVNHSRKEKQKRG 189  
 DB 286 IQLVAIPSPGELIYISDAKLRCVIVNL--PSDSLSVTWTRKSGNLRPDMVLOEHFNG 344  
 QY 190 TLVTSTLPVGTBMIEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVYMLPSPSEET 249  
 DB 345 TYSASAVPVSTQDMLSEGETYQVQHELPPLSKSVYRNTGTPTPLIYPPAPHPREL 404  
 QY 250 GTTR--TVCILRGFYPSSEISVQVLFNNEEDHTGHTTTPQKDH-----GTDPSFFLY 301  
 DB 405 SLSEVTLSCLVRGFRPRDIIRMDRAVATEFTTAVLPEERTANGAGDGDTPFFY 464  
 QY 302 SRMLVNSIKWKGMLVNCRVVHEALP---GSRITLXK 334  
 DB 465 SKMSVETAKMNGVTFVACMAVHEALPMRFSGRTLOK 500

RESULT 9

MBRM  
 Ig mu chain C region, membrane-bound form - rabbit  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 04-Dec-1986 #sequence\_revision 30-Jun-1991 #text\_change 23-Aug-1997  
 A/Accession: A02164  
 R/Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Magee, R.G.  
 J. Immunol. 132, 490-495, 1984  
 A/Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Haz 8  
 A/Reference number: A02164; MUID:84088930; PMID:6418803  
 A/Contents: a2 allotype  
 A/Accession: A02165  
 A/Molecule type: mRNA  
 A/Residues: 439-479 <BE2>  
 A/Accession: A02164  
 A/Molecule type: mRNA  
 A/Residues: 1-438, 'GRPTLVNLSIMDSTASTCY' <BER>  
 A/Note: the sequence of residue 1-438 was assumed to be identical with the corresponding C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:21-92/Domain: immunoglobulin homology <IMM1>  
 F:130-202/Domain: immunoglobulin homology <IMM2>  
 F:242-310/Domain: immunoglobulin homology <IMM3>  
 F:349-420/Domain: immunoglobulin homology <IMM4>  
 F:439-479/Domain: carboxyl-terminal <CTS>  
 F:14/Disulfide bonds: interchain (to light chain) #status predicted  
 F:28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted  
 F:46,114,261,277,284/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:1296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.8%; Score 497.5; DB 1; Length 479;  
 Best Local Similarity 32.9%; Pred. No. 6.4e-30;  
 Matches 117; Conservative 61; Mismatches 153; Indels 25; Gaps 10;

QY 5 HHHTLSPESGPV--TIPTPKLPHSSCDPR---GDAHSTITQLCLVSGSPAKVHT 59  
 DB 94 HSNRSRDLRVSPFVDSLPVSVF---IPRDSRSGSGTRKSLICQAGFSPKQSVS 150  
 QY 60 WLVDGGAEN--LPTTPRPGEGGQTFSLQSEVNTTQCGMMSNTYTCHVKNAGSIFE 116  
 DB 151 WLVDGGAEN--LPTTPRPGEGGQTFSLQSEVNTTQCGMMSNTYTCHVKNAGSIFE 116  
 QY 117 DS---SRKADSNPRGSAVLSRSPFDLTIKRSPTTCLVVDLAPSKGTVNLTWSPASG 173

DB 211 KNVMSSESTTPSPGICQVFPAPADTFISKARLCLVTDLT--TGSINISWASNG 269  
 QY 174 KPVNSTRKEKQKRGNTLTVTSTLPVGRDWTIEGTTCGRTHPHLPALMRSTTKLPK 233  
 DB 270 KALDTHMNTTSHPNATPSAMGEASVCAEDWESGQFTCTVTHADLPPLKHTISK--SR 327  
 QY 234 RLA---PEVYMLPSPER--TGTRTVCILRGFYPSSEISVQVLFNNEEDHTGHTTTP 288  
 DB 328 EVAKHPRAVYVLPARQQLIRBSATVTCVKGSPADIVQVQGPQSGQKVTYAP 387  
 QY 289 QKHGTDSFFLYSMVNSIKWKGMLVNCRVVHEALP---GSRITLXKSLHYSAG 341  
 DB 388 APEQAPGLYFTHSTLTVTEDMNSGFTTCVVGHEALPHWTERTVKSGTEGVEG 443

RESULT 10

MBRY  
 Ig mu chain C region - golden hamster  
 C/Species: Mesocricetus auratus (golden hamster)  
 C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Aug-1996  
 A/Accession: A02168  
 R/McGuire, K.L.; Duncan, W.R.; Tucker, P.W.  
 Nucleic Acids Res. 13, 5611-5628, 1985  
 A/Title: Phylogenetic conservation of immunoglobulin heavy chains: direct comparison of  
 A/Reference number: A02168; MUID:85297761; PMID:2994005  
 A/Accession: A02168  
 A/Molecule type: DNA  
 A/Residues: 1-454 <MCG>  
 A/Note: the sequence was determined from the germline gene  
 C/Genetics: 105/3; 218/3; 324/3  
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-90/Domain: immunoglobulin homology <IMM1>  
 F:128-200/Domain: immunoglobulin homology <IMM2>  
 F:238-306/Domain: immunoglobulin homology <IMM3>  
 F:345-416/Domain: immunoglobulin homology <IMM4>  
 F:445,112,139,192,210,238,257,280,326,441/Binding site: carbohydrate (Asn) (covalent) #  
 F:135-198,245-304,352-414/Disulfide bonds: #status predicted

Query Match 26.7%; Score 496; DB 1; Length 454;  
 Best Local Similarity 34.5%; Pred. No. 7.8e-30;  
 Matches 119; Conservative 60; Mismatches 150; Indels 16; Gaps 9;

QY 5 HHHTLSPESGPV--TIPTPKLPHSSCDPR---GDAHSTITQLCLVSGSPAKVHT 60  
 DB 91 HGNNTKDLRVDPG--VTENMNVSVFVPSRDAFGAPRKSRLFCESANSFSPKQITVSW 149  
 QY 61 LVDGGAENLFP---PTTPRPGEGGQTFSLQSEVNTTQCGMMSNTYTCHVKNAGSIFE 116  
 DB 150 LVDGGAENLFP---PTTPRPGEGGQTFSLQSEVNTTQCGMMSNTYTCHVKNAGSIFE 116  
 QY 117 DSRRKADSNPRGSAVLSRSPFDLTIKRSPTTCLVVDLAPSKGTVNLTWSPASGKPV 176  
 DB 210 NYSSTGAAPSRDIDAFPIPEFVGILPKSNTLCLVTLNLA--TYDTLINSWSSSGEPL 268  
 QY 177 NSTRKEKQKRGNTLTVTSTLPVGRDWTIEGTTCGRTHPHLPALMRSTTKLPK--KRL 235  
 DB 269 ETKTKLTSHPNATPSAMGEASVCAEDWESGQFTCTVTHADLPPLKHTISK--SR 327  
 QY 236 APEVYMLPSPER--TGTRTVCILRGFYPSSEISVQVLFNNEEDHTGHTTTP 288  
 DB 329 PRVYVQQLPARQQLIRBSATVTCVKGSPADIVQVQGPQSGQKVTYAP 387  
 QY 294 TTPSPFLYSRMLVNSIKWKGMLVNCRVVHEALP---GSRITLXKSLHYSAG 341  
 DB 389 APHLVYFTHSTLTVTEDMNSGFTTCVVGHEALPHWTERTVKSGTEGVEG 443

## RESULT 11

MHRB

Ig mu chain C region, secreted form - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 23-Aug-1997

C/Accession: A02164

R/Accession: K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.

J. Immunol. 132, 490-495, 1984

A/Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a

A/Reference number: A02164; MUID:8408930; PMID:6418803

A/Contents: a2 allotype

A/Accession: A02164

A/Molecule type: mRNA

A/Residues: 1-458 &lt;ER&gt;

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin

F/11-02/Domain: immunoglobulin homology &lt;IMM1&gt;

F/130-202/Domain: immunoglobulin homology &lt;IMM2&gt;

F/242-310/Domain: immunoglobulin homology &lt;IMM3&gt;

F/349-420/Domain: immunoglobulin homology &lt;IMM4&gt;

F/14/Disulfide bonds: interchain (to light chain) #status predicted

F/28-90,137-200,249-308,356-418/Disulfide bonds: #status predicted

F/46,114,212,261,277,284,445/Binding site: carbohydrate (Asn) (covalent) #status predicted

F/219,457/Disulfide bonds: interchain (to heavy chain) #status predicted

F/296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted

Query Match 26.7%; Score 495.5; DB 1; Length 458;

Best Local Similarity 33.1%; Pred. No. 8,6e-30;

Matches 116; Conservative 61; Mismatches 148; Indels 25; Gaps 10;

QY 5 HHHHTSLPESGQV--LIPPTVKLFHSSCDPR-----GDASHITOLCLVSGSPAKVAVT 59

DB 94 HSNNDRLVSPFVDSLPNVSF--LPPRDSGSGSTRSRILCOATGSPQJVSYS 150

QY 60 WLVDGQEAEN--LPEYTRPKREGQTFSLQSEVNTTQGMSSNTTYCHVKNISFE 116

DB 151 WLNDGQKVESGVLTKEVEAETKGAQATFSSMLTTESDWLSQSLVTCRDVHGIFPD 210

QY 117 DS---SRKCADSNPRVSAVLSRSPFDLFIKSPITITLVYDLAPSKGTNVLTSRASG 173

DB 211 KNVSMSECSSTPSPQIQLPPLAPSPADTFLSKARLCLVLDLT--TGSLSNTWSANG 269

QY 174 KPVNSTRKREKORNTLTVTSTLPYGTDWIEGTYQCRVTHPHLPALMSTKLPK 233

DB 270 KALDTMNTTSHPNATFSAAGASVCAEDWESGEFTCTVTHADLPPLKHTISK--SR 327

QY 234 RLA---PEYVMLPSPSE--TGTRVYTCILRGFYPSLSISVOMLNNEDHTGHTTRP 288

DB 328 EVAKHPAYVVLPAPEEQVLRASATVTCVKGFSADPVQWQORQPLSSDKYTSAP 387

QY 289 QXKHGDPSPFLTSRLVKNKSIWEKGNLTVCRVHAPL---GSRTLEKS 335

DB 388 APBPQAPGLVTHSTILVTEBDMNSGFTCTVGHGHALPHMTERIVDS 437

## RESULT 12

G2HU

Ig gamma-2 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000

C/Accession: A93906; A92809; A90752; A93132; A02168

R/Accession: J. J. Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A/Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con

A/Reference number: A93906; MUID:82197621; PMID:6804948

A/Accession: A93906

A/Molecule type: DNA

A/Residues: 1-326 &lt;ELL&gt;

A/Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:96066056

A/Note: Lys-326 is probably removed posttranslationally

R/Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A/Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and

A/Reference number: A92809; MUID:81007873; PMID:6774012

A/Contents: myeloma protein T11

A/Accession: A92809

A/Molecule type: protein

A/Residues: 1-119, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 &lt;MAN&gt;

A/Note: TYP-156 is at or near the complement-binding site

R/Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A/Title: The amino acid sequences of the three heavy chain constant region domains of a

A/Reference number: A90752; MUID:80001357; PMID:113060

A/Contents: myeloma protein Z1e

A/Accession: A90752

A/Molecule type: protein

A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198

A/Note: this sequence has since been revised

R/Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A/Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin

A/Reference number: A93132; MUID:80114419; PMID:118920

A/Contents: Z1e

A/Accession: A93132

A/Molecule type: protein

A/Residues: 238-275 &lt;HOP&gt;

R/Hofmann, T.; Parr, D.M.

submitted to the Atlas March 1980

A/Reference number: A94591

A/Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268

A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat

ned

R/Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A/Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.

A/Reference number: A90253; MUID:72033500; PMID:4940472

A/Contents: annotation; myeloma protein Sa, disulfide bonds

R/Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A/Title: Structural studies of immunoglobulin G.

A/Reference number: A93157; MUID:69064124; PMID:5782707

A/Contents: annotation; Sa, disulfide bonds

C/Genetics:

A/Gene: GDB:10HG2

A/Cross-references: GDB:119338; OMIM:147110

A/Map position: 14q32.33-14q33.33

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology &lt;IM1&gt;

F/133-202/Domain: immunoglobulin homology &lt;IM2&gt;

F/239-306/Domain: immunoglobulin homology &lt;IM3&gt;

F/14/Disulfide bonds: interchain (to light chain) #status experimental

F/127-83,140-200,246-304/Disulfide bonds: #status experimental

F/102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match 26.2%; Score 486.5; DB 1; Length 326;

Best Local Similarity 36.2%; Pred. No. 2.7e-29;

Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGDASHITOLCLVSGSPAKVAVT---LVVQGAENLFPYTRPKREGGTFSLQSE 90

DB 16 RSTSESTALGLVCKVDFPEPVVSNMAGLTG---VHTFPAVL---QSSGLVLSV 68

QY 91 VNITQGMSSNTTYCHVKR--NGSIFEDSSKCADSNP-----RGVSAYLSRPSF 140

DB 69 VVFPSSNF--GTQVYTCVNDHKPSNTKYDKVERKCCVCEGCPAPAPVAGSVLFPKPKR 127

QY 141 D-LFIRKSPITITLVYDLAPSKGTNVLTMGBASGKPVNSTRKEKORNGTLVTSPLPV 199

DB 128 DTLMISTRPEVYTCVVDVSHEDPEVQPMVYDGVYHNAKTREREGFNSTFRVSVLV 187

QY 200 GTRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPDEE-TGTRTYTCL 258  
 DB 188 VHQMWNKEKCKKCKVSNKGLPAIEKTSKTKGQPREQYVTLTPSPSEMTKQVSLTCL 247  
 QY 259 IRGYPSSISVQWLFNNEEDHTGHTTTPQKDHGTDPSFPLYSRMLVNSIWEKNLV 318  
 DB 248 VKGFPSDIAVEMESNGQPEN--NYKTPPMLD--SDGSFPLYSKLTVDKSRMOCQGVFS 303  
 QY 319 CRVVEHALPGSRITLTKSLHYASG 341  
 DB 304 CSVMHEALHNHYT-OKSLISLSPG 325

## RESULT 13

S25644  
 Ig mu chain C region - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 20-Feb-1995 #sequence\_revision 30-Jan-1998 #text\_change 21-Jan-2000  
 C:Accession: S25644  
 R:Parkes, K.; Bugeon, L.; Soullou, J.P.  
 submitted to the EMBL Data Library, September 1992  
 A:Reference number: S25644  
 A:Accession: S25644  
 A:Molecule type: mRNA  
 A:Residues: 1-343 <PAR>  
 A:Cross-references: EMBL:X68312; NID:G56461; PIDN:CAA6392.1; PID:9818025  
 A:Experimental source: spleen  
 C:Genetics:  
 A:Map position: 6  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:234-305/Domain: immunoglobulin homology <IMM>

Query Match 25.9%; Score 480.5; DB 2; Length 343;  
 Best Local Similarity 34.7%; Pred. No. 8e-29;  
 Matches 108; Conservative 59; Mismatches 131; Indels 13; Gaps 7;

QY 36 GDAHSTIQLCLVGSFSPAKVHTVMDVGEAENL---PYTPRKREGGQTFSEVN 92  
 DB 14 GPAPKSLICEATNFSKQITVSWLDGKPKGFTTEPYTAKSRPOTVIVITLT 73  
 QY 93 ITQGQWMSNTYTCVKNKNGSIF-EDSSRKCADSNPRGSAVLSRPSFPDLFIRKSPIT 151  
 DB 74 ITESPMILANFTCVDRGLTFWKNVSTCAASPTDILAFPIPRPADIFLTKAKLS 133  
 QY 152 CLVVDLARSKGTNLTWRSASGKPNHSTRKEKQKQNTLVITSLPGRDWTGEGTYQ 211  
 DB 134 CLVTMLA-TYDTLNTSWSSKSGEPLENTKIMESHPIGTFSAVGASVCEDMDNRKEFV 192  
 QY 212 CRVTHPLPALMRSTTKLPGK--RLAPEVYMLPPSPDEE-TGTRTYTCLIRGFYSEI 267  
 DB 193 CLVTHRDLPSPQKRIK-PNEVAKHPAVYLLPPARQQLIRSAVYTCGLVKFSPADI 251  
 QY 268 SVQWLFNNEEDHTGHTTTPQKDHGTDPSFPLYSRMLVNSIWEKNLVTCRVVEHALP 327  
 DB 252 FVQWLDQGPLSSDXYTSAPPEPGAGLYFTSHILVTVEEMNSGEYTCVVGHEALP 311

QY 328 ---GSRITLKS 335  
 DB 312 HMVTERITVDS 322

## RESULT 14

G4HU  
 Ig gamma-4 chain C region - human  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
 C:Accession: A90933; A90249; A02150  
 R:Ellison, J.; Buxbaum, J.; Hood, L.  
 DNA 1, 11-18, 1981  
 A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
 A:Reference number: A90933; MUID:83157104; PMID:6299662  
 A:Accession: A90933

A:Molecule type: DNA  
 A:Residues: 1-327 <EHL>  
 A>Note: the sequence was determined from the germ-line gene  
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
 Biochem. J. 117, 33-47, 1970  
 A>Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
 A:Reference number: A90249; MUID:70207560; PMID:4192699  
 A:Accession: A90249  
 A:Molecule type: protein  
 A:Residues: 1-30; 81-326 <PIN>  
 C:Genetics:  
 A:Gene: GDB:IGHG4  
 A:Cross-references: GDB:119340; OMIM:147130  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 99/1; 111/1; 221/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM2>  
 F:134-203/Domain: hinge  
 F:99-110/Region: hinge  
 F:240-307/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted  
 F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 476; DB 1; Length 327;  
 Best Local Similarity 35.8%; Pred. No. 1.7e-28;  
 Matches 116; Conservative 57; Mismatches 121; Indels 30; Gaps 10;

QY 35 RGDASTIQLCLVGSFSPAKVHTV---LVGGEAENLPYTPRKREGGQTFSEVN 90  
 DB 16 RSTSEITAGCLVXDYFPEPYTWSNGALTSQ---VHTPAVL---QSSGLTSLSV 68  
 QY 91 VNITQGWMSNTYTCVKNKNGSIFEDSSRKCADSNP-----RGVSAVLSRSP 139  
 DB 69 VIVPSS--LGTITTYCNDHDKPSNTKVDKVESKTKGFCPCSPAFELGSPVFLFPKP 127  
 QY 140 PD-LPIRSPPTTCLVVDLAPSKGTNLTWRSASGKPNHSTRKEKQKQNTLVITSLP 198  
 DB 128 KDTLMSRPREVTCVVVVSQEDPEVQFNWYDVGEVNAATKPREEOFNSTYRVVSLT 187  
 QY 199 VGRDWIEGETYQCRVTHPHLPALMRSTTKLPGKRLAPEVYMLPPSPDEE-TGTRTYTCL 257  
 DB 188 VHQWLNKEKCKKCKVSNKGLPSISTEIKTSKKGQPREQYVTLTPSPSEMTKQVSLTCL 247  
 QY 258 LIRGYPSSISVQWLFNNEEDHTGHTTTPQKDHGTDPSFPLYSRMLVNSIWEKNLV 317  
 DB 248 LVKGFPSDIAVEMESNGQPEN--NYKTPPMLD--SDGSFPLYSRLTVDKSRMOCQGVF 303  
 QY 318 TCrvVEHALPGSRITLTKSLHYASG 341  
 DB 304 CSVMHEALHNHYT-OKSLISLSPG 326

## RESULT 15

S14683  
 Ig mu chain precursor, membrane-bound (clone 201) - human  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
 C:Accession: S14683; S08047  
 R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.  
 Nucleic Acids Res. 18, 4278, 1990  
 A>Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain  
 A:Reference number: S14683; MUID:90332450; PMID:2115996  
 A:Accession: S14683  
 A:Molecule type: mRNA  
 A:Residues: 1-627 <FRI>  
 A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin; membrane protein

